

MON-0301.ST25.txt
SEQUENCE LISTING

<110> Monell Chemical Senses Center
Li, Xia
Li, Weihua
Reed, Danielle R.
Bachmanov, Alexander A.
Brand, Joseph G.

<120> TASTE RECEPTORS OF THE T1R FAMILY FROM DOMESTIC CAT

<130> MON-0301

<150> US 60/554,751
<151> 2004-03-19

<150> US 60/482,992
<151> 2003-06-27

<160> 99

<170> PatentIn version 3.2

<210> 1
<211> 2569
<212> DNA
<213> Felis catus

<400> 1
atgcccggcc tcgctctcct gggcctcacg gctctcctgg gcctcacggc tctcttggac 60
cacggggagg gcgcaacgtc ctgcttgcata cagcagctca ggatgcaggg ggactatgtg 120
ctgggtgggc tcttccctct gggctctgcc gagggtacag gtcttggcga cgggctgcag 180
cccaatgccca ccgtgtgcac caggttctcg tctctggcc tgctctggc gctggccgtg 240
aagatggcgg tggaggagat caacaacggg tcggccctgc tgcccgggct gcacctggc 300
tatgacctct ttgacacgtg ttcagagccc atggtgcca tgaagcccag cctcgtgttc 360
atggccaaag caggcagctg cagcattgcc gcctactgca attacacaca gtaccagccc 420
cgcgtgctgg ccgtcatcgg gccttactcg tctgagctcg ccctcgtcac cggcaagtcc 480
ttcagttct tccttgtgcc tcaggtcagc tacggcgcca gcaccgaccg gctgagcaac 540
cgggagatct tccccgtcctt cttccgcacg gtgcccagcg accaggtgca ggtggcggcc 600
atggtgagc tgctggagga gctcggtgg aactgggtgg cggcggtgg tagtgacgac 660
gagttatggcc ggcaggcccct gagcctttc tccggcctgg ccagcggccag gggcatctgc 720
atcgccgcatg agggcctggt gccactgccc ccaggcagcc tgccgttgg cgccctacag 780
ggcctgtgc gccaggtgaa ccagagcagc gtgcaggtgg tggtgctgtt ctccctcgcc 840
cacgcggccc gcaccctctt cagctacagc atccgctgca agctctcacc caaggtgtgg 900
gtggccagcg aggccctggct gacctcagac ctggtcata cgctgcccgg catgcctggg, 960
gtgggcaccc tgctggcctt cctgcagcag ggcggcccgta tgccggagtt cccatcctac 1020
gtgcggaccc gctggccctt ggccgctgac cctgccttct ggcctcgct ggacgctgaa 1080
cagccaggcc tggaggagca cgtgggtggg ccacgctgca cccaatgtga ccacgctcacg 1140
ctagagaacc tatctgcggg gctgctgcac caccagaccc tgcgtgccta cgccgtgtg 1200
tatggcgtgg cccaaaggccct tcacaacaca ctgcgtgcata atgcctcggtt ctgccccagg 1260

MON-0301.ST25.txt

| | | | | | | |
|-------------|-------------|-------------|--------------|-------------|-------------|------|
| cgggagcctg | tgccgcctg | gcagcccta | gagaacatgt | acaacgttag | cttccgtgct | 1320 |
| cgcggcctgg | caactgcagtt | cgacgccagc | ggaaacgtga | acgtggattt | cgacctgaaa | 1380 |
| ctgtgggtgt | ggcaggaccc | gacgcccag | ctgcgcaccg | taggcaccc | caaggccgc | 1440 |
| ctggagctct | ggcgctctca | gatgtgctgg | cacacgcgg | ggaaggcagca | gccccgtgtcc | 1500 |
| cagtgcctcc | ggcagtgcaa | ggaaggccag | gtgcgcgcg | tgaaggcctt | ccactcttgc | 1560 |
| tgttacaact | gcgtggactg | caaggcgggc | agttatcagc | gcaacccaga | tgaccccttc | 1620 |
| tgcacccagt | gtgaccagga | ccagtggctcc | ccagacccgg | gcacacgctg | cttcgcggc | 1680 |
| aagccatgt | tcctggcatg | gggggagcca | gctgtgctgc | tactgctcgc | gctgctggct | 1740 |
| ctggcgctgg | gcctggcgct | ggcagccctg | gggctttcc | tctggcactc | ggacagcccg | 1800 |
| ctgggttcagg | cctcagggtgg | gccacggggcc | tgctttggcc | tggcttgcc | gggcctggtc | 1860 |
| tgcctcagt | tcctccctgtt | ccctggccag | ccaggccctg | ccagctgcct | ggcccagcag | 1920 |
| ccactgttcc | accccccact | caactggctgc | ctgagcacgt | ttttcctgca | agccggccag | 1980 |
| atatttgtgg | gtcggagct | gccaccaagc | tgggctgaga | agatgcgtgg | ccgcctgcgg | 2040 |
| gggccttggg | cctggctgg | ggtgctgctt | gctatgctgg | cagaagccgc | attgtgtgcc | 2100 |
| tggtaacctgg | tagccttccc | gccagaggtg | gtgacggact | ggcgggtact | gcccacagag | 2160 |
| gcgctgggtgc | actgccacgt | gcactccctgg | atcagcttcg | gcctggtgca | tgccactaac | 2220 |
| ccatgctgg | cctccctctg | cttcctgggc | actttcctgg | tgcagagccg | gccaggccgc | 2280 |
| tacaatggtg | cccgccgcct | caccttgcc | atgctggcct | acttcatcac | ctggatctcc | 2340 |
| tttgtgcccc | tcttgccaa | tgtgcacgtg | gcctaccagc | ctgcccgtgca | gatgggcacc | 2400 |
| atcctctct | gtgccttggg | tatcctagcc | accccttccacc | tgccttggg | ctacctgctg | 2460 |
| ctgcagcggc | cggagctcaa | cacccctgag | ttcttcctgg | aagacaatgc | cagagcacag | 2520 |
| ggcagcagtt | ggggcaggg | gaggggagaa | tcggggcaaa | aacaagtga | | 2569 |

<210> 2
<211> 865
<212> PRT
<213> Felis catus

<400> 2

Met Pro Gly Leu Ala Leu Leu Gly Leu Thr Ala Leu Leu Gly Leu Thr
1 5 10 15

Ala Leu Leu Asp His Gly Glu Gly Ala Thr Ser Cys Leu Ser Gln Gln
20 25 30

Leu Arg Met Gln Gly Asp Tyr Val Leu Gly Gly Leu Phe Pro Leu Gly
35 40 45

Ser Ala Glu Gly Thr Gly Leu Gly Asp Gly Leu Gln Pro Asn Ala Thr
50 55 60

Val Cys Thr Arg Phe Ser Ser Leu Gly Leu Leu Trp Ala Leu Ala Val

MON-0301.ST25.txt

| | | | |
|---|-----|-----|-----|
| 65 | 70 | 75 | 80 |
| Lys Met Ala Val Glu Glu Ile Asn Asn Gly Ser Ala Leu Leu Pro Gly | | | |
| 85 | 90 | 95 | |
| Leu His Leu Gly Tyr Asp Leu Phe Asp Thr Cys Ser Glu Pro Met Val | | | |
| 100 | 105 | 110 | |
| Ala Met Lys Pro Ser Leu Val Phe Met Ala Lys Ala Gly Ser Cys Ser | | | |
| 115 | 120 | 125 | |
| Ile Ala Ala Tyr Cys Asn Tyr Thr Gln Tyr Gln Pro Arg Val Leu Ala | | | |
| 130 | 135 | 140 | |
| Val Ile Gly Pro His Ser Ser Glu Leu Ala Leu Val Thr Gly Lys Phe | | | |
| 145 | 150 | 155 | 160 |
| Phe Ser Phe Phe Leu Val Pro Gln Val Ser Tyr Gly Ala Ser Thr Asp | | | |
| 165 | 170 | 175 | |
| Arg Leu Ser Asn Arg Glu Ile Phe Pro Ser Phe Phe Arg Thr Val Pro | | | |
| 180 | 185 | 190 | |
| Ser Asp Gln Val Gln Val Ala Ala Met Val Glu Leu Leu Glu Glu Leu | | | |
| 195 | 200 | 205 | |
| Gly Trp Asn Trp Val Ala Ala Val Gly Ser Asp Asp Glu Tyr Gly Arg | | | |
| 210 | 215 | 220 | |
| Gln Gly Leu Ser Leu Phe Ser Gly Leu Ala Ser Ala Arg Gly Ile Cys | | | |
| 225 | 230 | 235 | 240 |
| Ile Ala His Glu Gly Leu Val Pro Leu Pro Pro Gly Ser Leu Arg Leu | | | |
| 245 | 250 | 255 | |
| Gly Ala Leu Gln Gly Leu Leu Arg Gln Val Asn Gln Ser Ser Val Gln | | | |
| 260 | 265 | 270 | |
| Val Val Val Leu Phe Ser Ser Ala His Ala Ala Arg Thr Leu Phe Ser | | | |
| 275 | 280 | 285 | |
| Tyr Ser Ile Arg Cys Lys Leu Ser Pro Lys Val Trp Val Ala Ser Glu | | | |
| 290 | 295 | 300 | |
| Ala Trp Leu Thr Ser Asp Leu Val Met Thr Leu Pro Gly Met Pro Gly | | | |
| 305 | 310 | 315 | 320 |
| Val Gly Thr Val Leu Gly Phe Leu Gln Gln Gly Ala Pro Met Pro Glu | | | |
| 325 | 330 | 335 | |
| Phe Pro Ser Tyr Val Arg Thr Arg Leu Ala Leu Ala Ala Asp Pro Ala | | | |
| 340 | 345 | 350 | |

MON-0301.ST25.txt

Phe Cys Ala Ser Leu Asp Ala Glu Gln Pro Gly Leu Glu Glu His Val
355 360 365

Val Gly Pro Arg Cys Pro Gln Cys Asp His Val Thr Leu Glu Asn Leu
370 375 380

Ser Ala Gly Leu Leu His His Gln Thr Phe Ala Ala Tyr Ala Ala Val
385 390 395 400

Tyr Gly Val Ala Gln Ala Leu His Asn Thr Leu Arg Cys Asn Ala Ser
405 410 415

Gly Cys Pro Arg Arg Glu Pro Val Arg Pro Trp Gln Leu Leu Glu Asn
420 425 430

Met Tyr Asn Val Ser Phe Arg Ala Arg Gly Leu Ala Leu Gln Phe Asp
435 440 445

Ala Ser Gly Asn Val Asn Val Asp Tyr Asp Leu Lys Leu Trp Val Trp
450 455 460

Gln Asp Pro Thr Pro Glu Leu Arg Thr Val Gly Thr Phe Lys Gly Arg
465 470 475 480

Leu Glu Leu Trp Arg Ser Gln Met Cys Trp His Thr Pro Gly Lys Gln
485 490 495

Gln Pro Val Ser Gln Cys Ser Arg Gln Cys Lys Glu Gly Gln Val Arg
500 505 510

Arg Val Lys Gly Phe His Ser Cys Cys Tyr Asn Cys Val Asp Cys Lys
515 520 525

Ala Gly Ser Tyr Gln Arg Asn Pro Asp Asp Leu Leu Cys Thr Gln Cys
530 535 540

Asp Gln Asp Gln Trp Ser Pro Asp Arg Ser Thr Arg Cys Phe Ala Arg
545 550 555 560

Lys Pro Met Phe Leu Ala Trp Gly Glu Pro Ala Val Leu Leu Leu
565 570 575

Ala Leu Leu Ala Leu Ala Leu Gly Leu Ala Leu Ala Ala Leu Gly Leu
580 585 590

Phe Leu Trp His Ser Asp Ser Pro Leu Val Gln Ala Ser Gly Gly Pro
595 600 605

Arg Ala Cys Phe Gly Leu Ala Cys Leu Gly Leu Val Cys Leu Ser Val
610 615 620

Leu Leu Phe Pro Gly Gln Pro Gly Pro Ala Ser Cys Leu Ala Gln Gln

MON-0301.ST25.txt

| | | | |
|-----|-----|-----|-----|
| 625 | 630 | 635 | 640 |
|-----|-----|-----|-----|

Pro Leu Phe His Leu Pro Leu Thr Gly Cys Leu Ser Thr Phe Phe Leu
645 650 655

Gln Ala Ala Glu Ile Phe Val Gly Ser Glu Leu Pro Pro Ser Trp Ala
660 665 670

Glu Lys Met Arg Gly Arg Leu Arg Gly Pro Trp Ala Trp Leu Val Val
675 680 685

Leu Leu Ala Met Leu Ala Glu Ala Ala Leu Cys Ala Trp Tyr Leu Val
690 695 700

Ala Phe Pro Pro Glu Val Val Thr Asp Trp Arg Val Leu Pro Thr Glu
705 710 715 720

Ala Leu Val His Cys His Val His Ser Trp Ile Ser Phe Gly Leu Val
725 730 735

His Ala Thr Asn Ala Met Leu Ala Phe Leu Cys Phe Leu Gly Thr Phe
740 745 750

Leu Val Gln Ser Arg Pro Gly Arg Tyr Asn Gly Ala Arg Gly Leu Thr
755 760 765

Phe Ala Met Leu Ala Tyr Phe Ile Thr Trp Ile Ser Phe Val Pro Leu
770 775 780

Phe Ala Asn Val His Val Ala Tyr Gln Pro Ala Val Gln Met Gly Thr
785 790 795 800

Ile Leu Leu Cys Ala Leu Gly Ile Leu Ala Thr Phe His Leu Pro Lys
805 810 815

Cys Tyr Leu Leu Leu Gln Arg Pro Glu Leu Asn Thr Pro Glu Phe Phe
820 825 830

Leu Glu Asp Asn Ala Arg Ala Gln Gly Ser Ser Trp Gly Gln Gly Arg
835 840 845

Gly Glu Ser Gly Gln Lys Gln Val Thr Pro Asp Pro Val Thr Ser Pro
850 855 860

Gln
865

<210> 3
<211> 2532
<212> DNA
<213> Mus musculus

<400> 3
atgggacccc aggcgaggac actccatttg ctgtttctcc tgctgcatgc tctgcctaag 60

MON-0301.ST25.txt

| | | | | | | | |
|--------------|------------|-------------|-------------|-------------|------------|------------|------|
| ccagtcatgc | tggtagggaa | ctccgacttt | cacctggctg | gggactacct | cctgggtggc | 120 | |
| ctctttaccc | tccatgccaa | cgtgaagagc | gtctctcacc | tcagctacct | gcaggtgcc | 180 | |
| aagtgcata | agtacaacat | gaaggcttg | ggctacaacc | tcatgcaggc | catgcattc | 240 | |
| gccgtggagg | aatcaacaa | ctgtagctct | ctgctgccc | gcgtgctgct | cggctacgag | 300 | |
| atggtggatg | tctgctaccc | ctccaacaat | atccagcctg | ggctctactt | cctgtcacag | 360 | |
| atagatgact | tcctgccc | cctcaaagac | tacagccagt | acaggcccc | agtggtggcc | 420 | |
| gtcattggcc | cagacaactc | tgagtccgccc | atcaccgtgt | ccaacattct | ctcctacttc | 480 | |
| ctcgtgccac | aggtcacata | taggccatc | accgacaaggc | tgcgagacaa | gcggcgcttc | 540 | |
| cctgcccattgc | tgcgactgt | gcccagcgcc | acccaccaca | tcgaggccat | ggtcaactg | 600 | |
| atggttca | tccagtggaa | ctggatcg | gtgctggta | gcgatgacga | ttatggccga | 660 | |
| gagaacagcc | acctgctgag | ccagcgtctg | accaacactg | gcgatatctg | cattgccttc | 720 | |
| caggaggttc | tgcgtgtacc | agaacccaac | caggccgtga | ggcctgagga | gcaggacaa | 780 | |
| ctggacaaca | tcctggacaa | gctgcccgg | acctcgccgc | gtgtggtgt | gatattctcg | 840 | |
| ccagagctga | gcctgcacaa | cttctccgc | gaggtgctgc | gctggaaactt | cacaggcttt | 900 | |
| gtgtggattg | cctctgagtc | ctggccatc | gaccctgttc | tacacaacct | cacagagctg | 960 | |
| cgccacacgg | gcactttcct | gggcgtcacc | atccagaggg | tgtccatccc | tggcttcagc | 1020 | |
| cagttccgag | tgcgccacga | caagccagag | tatccatgc | ctaacgagac | cagcctgagg | 1080 | |
| actacctgta | accaggactg | tgacgcctgc | atgaacatca | ccgagtcc | taacaacgtt | 1140 | |
| ctcatgcttt | cggggagcg | tgtggtctac | agtgtgtact | cggccgtcta | cgcgttagcc | 1200 | |
| cacaccctcc | acagactcct | ccactgcaac | caggtccgct | gcaccaagca | aatcgtctat | 1260 | |
| ccatggcagc | tactcaggga | gatctggcat | gtcaacttca | cgctcctgg | caaccagctc | 1320 | |
| ttcttcgacg | aacaagggga | catgccatg | ctcctggaca | tcatccagt | gcaatggggc | 1380 | |
| ctgagccaga | acccttcca | aagcatcgcc | tcctactccc | ccaccgagac | gaggctgacc | 1440 | |
| tacattagca | atgtgtcctg | gtacacccccc | aacaacacgg | tcccccata | catgtgttct | 1500 | |
| aagagttgcc | agcctggca | aatgaaaaaa | cccataggcc | tccaccctgt | ctgcttcag | 1560 | |
| tgtgtggact | gtccgcccgg | cacctacctc | aaccgatcag | tagatgagtt | taactgtctg | 1620 | |
| tcctgcccgg | gttccatgtg | gtcttacaag | aacaacatcg | cttgc | tcgcccgt | 1680 | |
| gccttcctgg | agtggcacga | agtgc | ccactgtgt | ccatcctggc | cgcctggc | 1740 | |
| ttcatcagta | cgctggccat | tctgctcatc | ttctggagac | at | ttccagac | gcccattgt | 1800 |
| cgctcggcgg | gccc | gtgcttcctg | atgctggtgc | ccctgctgct | ggcgttccgg | 1860 | |
| atggtccccg | tgtatgtggg | ccccccacg | gtcttctcct | gtttctgccc | ccaggcttcc | 1920 | |
| ttcacccgtt | gttctccgt | ctgcctctcc | tgcac | tgcgttcc | ccagattgt | 1980 | |
| tgcgttca | agatggccag | acgcctgcca | agcgcctacg | gtttctggat | gcgttaccac | 2040 | |
| ggccctacg | tctt | gtggc | cttcatcag | gccgtcaagg | tggccctgg | ggcaggcaac | 2100 |
| atgctggcca | ccaccatcaa | ccccattggc | cggaccgacc | ccgatgaccc | caatatcata | 2160 | |

MON-0301.ST25.txt

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| atcctctcct | gccaccctaa | ctaccgcaac | gggctactct | tcaacaccag | catggacttg | 2220 |
| ctgctgtccg | tgctgggttt | cagcttcgcg | tacgtggca | aggaactgcc | caccaactac | 2280 |
| aacgaagcca | agttcatcac | cctcagcatg | accttctcct | tcacccctc | catctccctc | 2340 |
| tgcacgttca | tgtctgtcca | cgatggcgtg | ctggcacca | tcatggatct | cctggtcact | 2400 |
| gtgctcaact | ttctggccat | cggcttgggg | tactttggcc | ccaagtgtta | catgatcctt | 2460 |
| ttctaccgg | agcgcaacac | ttcagcttat | ttcaatagca | tgattcaggg | ctacacgatg | 2520 |
| aggaagagct | ag | | | | | 2532 |

<210> 4
<211> 2529
<212> DNA
<213> Rattus rattus

| | | | | | | |
|-------------|-------------|-------------|------------|-------------|-------------|------|
| <400> 4 | | | | | | |
| atgggtcccc | aggcaaggac | actctgcttg | ctgtctctcc | tgctgcatgt | tctgcctaag | 60 |
| ccaggcaagc | tggttagagaa | ctctgacttc | cacctggccg | gggactacct | cctgggtggc | 120 |
| ctctttaccc | tccatgccaa | cgtgaagagc | atctcccacc | tcatgtaccc | gcaggtgccc | 180 |
| aagtgcata | gttccaccat | gaagggttg | ggctacaacc | tcatgcaggc | catgcgtttc | 240 |
| gctgtggagg | agatcaacaa | ctgtagctcc | ctgctaccgg | gcgtgtcgct | cggctacgag | 300 |
| atgggtggatg | tctgttaccc | ctccaaacaat | atccaccctg | ggctctactt | cctggcacag | 360 |
| gacgacgacc | tcctgcccatt | cctcaaagac | tacagccagt | acatgccttca | cgtgggtggct | 420 |
| gtcattggcc | ccgacaactc | ttagtccgccc | attaccgtgt | ccaacattct | ctctcatttc | 480 |
| ctcatccac | agatcacata | cagcgcattc | tccgacaago | tgcgggacaa | gcggcacttc | 540 |
| cctagcatgc | tacgcacagt | gcccagcgcc | accaccaca | tgcaggccat | ggtgcagctg | 600 |
| atgggttcact | tccaatggaa | ctggattgtg | gtgctggta | gcgacgacga | ttacggccgc | 660 |
| gagaacagcc | acctgtttag | ccagcgtctg | acccaaacga | gcgacatctg | cattgccttc | 720 |
| caggaggttc | tgcccatacc | ttagtccagc | caggtcatga | ggtccgagga | gcagagacaa | 780 |
| ctggacaaca | tcctggacaa | gctgcggccg | acctcgccgc | gcgtcggtgt | ggtgttctcg | 840 |
| cccgagctga | gcctgtatag | cttcttcac | gaggtgctcc | gctggaaactt | cacgggtttt | 900 |
| gtgtggatcg | cctctgagtc | ctgggtatcc | gaccctgttc | tgcataacct | cacggagctg | 960 |
| cgccacacgg | gtactttct | gggcgtcacc | atccagaggg | tgtccatccc | tggcttcagt | 1020 |
| cagttccgag | tgcgcgtga | caagccaggg | tatcccgtgc | ctaacacgac | caacctgcgg | 1080 |
| acgacactgca | accaggactg | tgacgcctgc | ttgaacacca | ccaagtccctt | caacaacatc | 1140 |
| cttatacttt | cgggggagcg | cgtggtctac | agcgtgtact | cggcagttta | cgcgggtggcc | 1200 |
| catgccctcc | acagactcct | cggctgtaac | cgggtccgct | gcaccaagca | aaaggtctac | 1260 |
| ccgtggcagc | tactcaggga | gatctggcac | gtcaacttca | cgctcctggg | taaccggctc | 1320 |
| ttctttgacc | aacaagggga | catgccgatg | ctcttggaca | tcatccagtg | gcagtgggac | 1380 |
| ctgagccaga | atcccttcca | aagcatcgcc | tcctattctc | ccaccagcaa | gaggctaacc | 1440 |

MON-0301.ST25.txt

| | | | | | | |
|-------------|------------|-------------|-------------|------------|------------|------|
| tacattaaca | atgtgtcctg | gtacacccccc | aacaacacgg | tccctgtctc | catgtgttcc | 1500 |
| aagagactgcc | agccagggc | aataaaaaag | tctgtggcc | tccacccttg | ttgcttcgag | 1560 |
| tgcttggatt | gtatgccagg | cacctacctc | aaccgctcag | cagatgagtt | taactgtctg | 1620 |
| tcctgccccgg | gttccatgtg | gtcctacaag | aacgacatca | cttgcttcca | gcggcggcc | 1680 |
| accttcctgg | agtggcacga | agtcccacc | atcggtgg | ccatactggc | tgccctggc | 1740 |
| ttcttcagta | cactggccat | tctttcatac | ttctggagac | atttccagac | acccatggtg | 1800 |
| cgctcggccg | gtggccccc | atgtccctg | atgcgtgc | ccctgctgct | ggcgtttgg | 1860 |
| atgggtccccg | tgtatgtggg | gccccccacg | gtcttcata | gtttctgc | acaggcttc | 1920 |
| ttcacccgtct | gtttctccat | ctgcctatcc | tgcatacaccg | tgcgctcctt | ccagatcg | 1980 |
| tgtgtcttca | agatggccag | acgcctgcca | agtgcctaca | gtttttggat | gcgttaccac | 2040 |
| gggcctatg | tcttcgtggc | cttcatacag | gccatcaagg | tggccctgg | ggtgggcaac | 2100 |
| atgctggcca | ccaccatcaa | ccccattggc | cggaccgacc | cggatgaccc | caacatcatg | 2160 |
| atcctctcg | gccaccctaa | ctaccgcaac | gggctactgt | tcaacaccag | catggactt | 2220 |
| ctgctgtctg | tgctgggttt | cagcttcgct | tacatggca | aggagctgc | caccaactac | 2280 |
| aacgaagcca | agttcatcac | tctcagcatg | accttctcct | tcacccctc | catctccctc | 2340 |
| tgcaccttca | tgtctgtgca | cgacggcg | ctggcacca | tcatggacct | cctggta | 2400 |
| gtgctcaact | tcctggccat | cggcttgg | tactttggc | ccaagtgtt | catgatcctt | 2460 |
| ttctacccgg | agcgcaacac | ctcagcctat | ttcaatagca | tgtccagg | ctacaccatg | 2520 |
| aggaagagc | | | | | | 2529 |

<210> 5
<211> 2520
<212> DNA
<213> Homo sapiens

<400> 5
atggggccca gggcaaagac catctgctcc ctgttcttcc tcctatgggt cctggctgag 60
ccggctgaga actcgactt ctacctgcct gggattacc tcctgggtgg cctcttctcc 120
ctccatgcca acatgaaggg cattgttacac cttaacttcc tgcaggtgcc catgtgcaag 180
gagtatgaag tgaagggtat aggctacaac ctcatacgagg ccatgcgtt cgccgtggag 240
gagatcaaca atgacagcag cctgctgcct ggtgtgctgc tggctatga gatcgtggat 300
gtgtgctaca tctccaacaa tgtccagccg gtgctctact tcctggcaca cgaggacaac 360
ctccttccca tccaagagga ctacagtaac tacatttccc gtgtggtggc tgtcattggc 420
cctgacaact ccgagtctgt catgactgtg gccaaacttcc tctccctatt tctcccttcca 480
cagatcacct acagcgccat cagcgatgag ctgcgagaca aggtgcgtt cccggctttg 540
ctgcgtacca cacccagcgc cgaccaccac gtcgaggcga tggcagact gatgctgcac 600
ttccgctgga actggatcat tgtgctggtg agcagcgcaca cctatggccg cgacaatggc 660
cagctgcttg gcgagcgcgt ggcccgccgc gacatctgca tcgccttcca ggagacgcgt 720
cccacactgc agcccaacca gaacatgacg tcagaggagc gccagcgcct ggtgaccatt 780

MON-0301.ST25.txt

| | | | | | | |
|-------------|-------------|-------------|-------------|-------------|------------|------|
| gtggacaagg | tgcagcagag | cacagcgcc | gtcgtggcg | tgttctcgcc | cgacctgacc | 840 |
| ctgttaccact | tcttcaatga | ggtgctgcgc | cagaacttca | cgggcgccgt | gtggatcgcc | 900 |
| tccgagtcct | gggcatcgaa | cccggtcctg | cacaacctca | cggagctggg | ccacttgggc | 960 |
| accttccctgg | gcatcaccat | ccagagcgtg | ccatcccgg | gcttcagtga | gttccgcgag | 1020 |
| tggggccac | aggctgggcc | gccacccctc | agcaggacca | gccagagcta | tacctgcaac | 1080 |
| caggagtgcg | acaactgcct | gaacgccacc | ttgtccttca | acaccattct | caggctctct | 1140 |
| ggggagcgtg | tctgtctacag | cgtgtactct | gccccatcg | ctgtggccca | tgccctgcac | 1200 |
| agcctccctcg | gctgtgacaa | aagcacctgc | accaagaggg | tggtctaccc | ctggcagctg | 1260 |
| ctttaggaga | tctgaaagg | caacttca | ctccctggacc | accaaatttt | cttcgaccgg | 1320 |
| caaggggacg | tggctctgca | cttggagatt | gtccagtggc | aatgggaccg | gagccagaat | 1380 |
| cccttccaga | gcgtcgccctc | ctactacccc | ctgcagcgc | agctgaagaa | catccaagac | 1440 |
| atctcctggc | acaccgtcaa | caacacgatc | cctatgtcca | tgtgttccaa | gaggtgccag | 1500 |
| tcagggcaaa | agaagaagcc | tgtggcata | cacgtctgt | gcttcgagtg | catcgactgc | 1560 |
| cttccggca | ccttcctcaa | ccacactgaa | gatgaatatg | aatgccaggc | ctgcccgaat | 1620 |
| aacgagtgg | cctaccagag | tgagacctcc | tgcttcaagc | ggcagctgg | cttcctggaa | 1680 |
| tggcatgagg | cacccaccat | cgctgtggcc | ctgctggccg | ccctgggctt | cctcagcacc | 1740 |
| ctggccatcc | tggatatt | ctggaggcac | ttccagacac | ccatagttcg | ctcggctgg | 1800 |
| ggccccatgt | gcttcctgat | gctgacactg | ctgctggtg | catacatgg | ggtcccgg | 1860 |
| tacgtggggc | cgcggaaagg | ctccacctgc | ctctggcc | aggccctt | tccctctgc | 1920 |
| ttcacaattt | gcatctcctg | tatcgccgt | cggtttcc | agatcgctg | cgccttcaag | 1980 |
| atggccagcc | gcttcccacg | cgcctacagc | tactgggtcc | gctaccaggg | gccctacgtc | 2040 |
| tctatggcat | ttatcacgg | actcaaaatg | gtcattgtgg | taattggcat | gctggccacg | 2100 |
| ggcctcagtc | ccaccacccg | tactgacccc | gatgacccca | agatcacaat | tgttcctgt | 2160 |
| aaccccaact | accgcaacag | cctgctgttc | aacaccagcc | tggacctgct | gctctcagtg | 2220 |
| gtgggttca | gttcgccta | catggcaaa | gagctgccc | ccaaactacaa | cgaggccaag | 2280 |
| ttcatcaccc | ttagcatgac | cttcttatttc | acccatccg | tctccctctg | cacccatg | 2340 |
| tctgcctaca | gcgggggtgc | ggtcaccatc | gtggacctct | tggtactgt | gctcaacctc | 2400 |
| ctggccatca | gcctgggcta | cttcggccccc | aagtgctaca | tgatcctt | ctacccggag | 2460 |
| cgcaacacgc | ccgcctactt | caacagcatg | atccagggt | acaccatgag | gagggactag | 2520 |

<210> 6
<211> 2529
<212> DNA
<213> Mus musculus

| | | | | | | |
|------------|------------|------------|-----------|------------|------------|-----|
| <400> 6 | | | | | | |
| atgcctttct | ggcagctca | cctgctgc | agcctgc | tggccgttgc | ttactgctgg | 60 |
| gctttcagct | gccaaaggac | agaatcctct | ccaggttca | gcctccctgg | ggacttcctc | 120 |

| MON-0301.ST25.txt | |
|-------------------|------|
| ctggcaggcc | 180 |
| tgttctccct | |
| ccatgtcgac | |
| tgttgtcgagg | |
| tgagacacag | |
| acctctggtg | |
| acaaggttgt | 240 |
| acaggtctga | |
| cagctcaac | |
| ggccatggct | |
| atcacctctt | |
| ccaagccatg | |
| cggttcaccg | 300 |
| ttgaggagat | |
| aaacaactcc | |
| acagctctgc | |
| ttcccaacat | |
| caccctgggg | |
| tatgaactgt | 360 |
| atgacgtgtg | |
| ctcagagtct | |
| tccaatgtct | |
| atgccaccct | |
| gagggtgctc | |
| gcccagcaag | 420 |
| ggacaggcca | |
| cctagagatg | |
| cagagagatc | |
| ttcgcaacca | |
| ctccctccaag | |
| gtggtggcac | 480 |
| tcattgggcc | |
| tgataaacact | |
| gaccacgctg | |
| tcaccactgc | |
| tgccctgctg | |
| agcccttttc | 540 |
| tgtatgcccct | |
| ggtcagctat | |
| gaggcgagca | |
| gcgtgtatcct | |
| cagtgaaaag | |
| cgcaagttcc | 600 |
| cgtccttctt | |
| gcmcaccatc | |
| cccagcgata | |
| agtaccaggt | |
| ggaagtcat | |
| gtgcggctgc | 660 |
| tgcagagctt | |
| cggctgggtc | |
| tggatctcgc | |
| tcgttggcag | |
| ctatggtgc | |
| tacgggcagc | 720 |
| tgggcgtaca | |
| ggcgctggag | |
| gagctggcca | |
| ctccacgggg | |
| catctgcgtc | |
| gccttcaagg | 780 |
| acgtggtgcc | |
| tctctccgcc | |
| caggcgggtg | |
| acccaaggat | |
| gcagcgcata | |
| atgctgcgtc | 840 |
| tggctcgagc | |
| caggaccacc | |
| gtggtcgtgg | |
| tcttctctaa | |
| ccggcacctg | |
| gctggagtgt | 900 |
| tcttcagggtc | |
| tgtggtgctg | |
| gccaacctga | |
| ctggcaaagt | |
| gtggatcgcc | |
| tccgaagact | 960 |
| gggccccatctc | |
| cacgtacatc | |
| accaatgtgc | |
| ccgggatcca | |
| gggcattggg | |
| acggtgctgg | 1020 |
| gggtggccat | |
| ccagcagaga | |
| caagtccctg | |
| gcctgaagga | |
| gtttgaagag | |
| tcctatgtcc | 1080 |
| aggcagtgtat | |
| gggtgctccc | |
| agaacttgcc | |
| cagaggggtc | |
| ctgggtgcggc | |
| actaaccagc | 1140 |
| tgtgcaggga | |
| gtgtcagct | |
| ttcacgacat | |
| ggaacatgcc | |
| cgagcttgga | |
| gccttctcca | 1200 |
| tgagcgctgc | |
| ctacaatgtg | |
| tatgaggctg | |
| tgtatgctgt | |
| ggcccacggc | |
| ctccaccagc | 1260 |
| tcctggatg | |
| tacctctggg | |
| acctgtgcc | |
| gaggcccagt | |
| ctacccctgg | |
| cagcttcttc | 1320 |
| agcagatcta | |
| caaggtgaat | |
| ttccttctac | |
| ataagaagac | |
| tgttagcattc | |
| gatgacaagg | 1380 |
| gggaccctct | |
| aggttattat | |
| gacatcatcg | |
| cctggactg | |
| aatggacact | |
| aatggacact | 1440 |
| ttgaggtcat | |
| tggttctgcc | |
| tcactgtctc | |
| cagttcatct | |
| agacataaat | |
| aagacaaaaaa | 1500 |
| tccagtgcc | |
| cgggaaagaac | |
| aatcagggtc | |
| ctgtgtcagt | |
| gtgtaccagg | |
| gactgtctcg | 1560 |
| aagggcacca | |
| caggttggtc | |
| atgggttccc | |
| accactgctg | |
| cttcgagtgc | |
| atgccctgtg | 1620 |
| aagctggac | |
| atttctcaac | |
| acgagtgtgc | |
| ttcacacactg | |
| ccagccttgt | |
| ggaacagaag | 1680 |
| aatggggcccc | |
| tgaggggagc | |
| tcagcctgct | |
| tctcacgcac | |
| cgtggagttc | |
| ttgggggtgc | 1740 |
| atgaacccat | |
| ctctttggtg | |
| ctattagcag | |
| ctaacacgct | |
| attgctgtcg | |
| ctgctgattg | 1800 |
| ggactgtctg | |
| cctgttgcc | |
| tggcgcttcc | |
| acacgcctgt | |
| tgtgaggtca | |
| gctggggta | 1860 |
| ggctgtgctt | |
| cctcatgctg | |
| ggttccttgg | |
| tagctggag | |
| ttgcagcctc | |
| tacagttct | 1920 |
| tcgggaagcc | |
| cacggtgc | |
| gcgtgtctgc | |
| tgcgtcagcc | |
| cctctttct | |
| ctcgggtttg | 1980 |
| ccattttcct | |
| ctcctgtctg | |
| acaatccgct | |
| ccttccaact | |
| ggtcatcatc | |
| ttcaagtttt | 2040 |
| ctaccaaggt | |
| acccacattc | |
| taccacactt | |
| gggccccaaa | |
| ccatggtgcc | |
| ggaatattcg | 2100 |
| tcattgtcag | |
| ctccacggtc | |
| catttgttcc | |
| tctgtctcac | |
| gtggcttgca | |
| atgtggaccc | 2160 |
| cacggccccac | |
| cagggagttac | |
| cagcgcttcc | |
| cccacatctgt | |
| gatttttgag | |
| tgcacagagg | 2220 |
| tcaactctgt | |
| gggcttcctg | |
| gtggctttcg | |
| cacacaacat | |
| cctctcttc | |

```
<210>    7
<211> 2520
<212> DNA
<213> Rattus rattus
```

<400> 7
atgctcttct gggctgctca cctgctgctc agcctgcagt tggtctactg ctgggctttc 60
agctgccaaa ggacagagtc ctctccaggc tttagcccttc ctggggactt ctccttgca
ggtctgttct ccctccatgg tgactgtctg caggtgagac acagacctct ggtgacaagt 120
tgtgacaggc ccgacagctt caacggccat ggctaccacc tcttccaagc catcggttc
actgttgagg agataaaacaa ctccctggcc ctgcttccca acatcacccct ggggtatgag 180
ctgtacgacg tgtgctcaga atctgccaat gtgtatgcca ccctgaggggt gcttgcctg
caagggcccc gccacataga gatacagaaa gacccctcgca accactccctc caaggtggtg 240
gccttcatcg ggcctgacaa cactgaccac gctgtcacta ccgctgcctt gctgggtcct 300
ttccctgatgc ccctggtcag ctatgaggca agcagcgtgg tactcagtgca caagcgcaag 360
ttcccgtctt tccttcgtac cgccccagt gaccggcacc aggtggaggt catggtgca 420
ctgctgcaga gtttgggtg ggtgtggatc tcgctcatttgcagctacgg tgattacggg
cagctgggtg tgcaggcgct ggaggagctg gccgtgcccc ggggcatctg cgtcgccttc 480
aaggacatcg tgccttctc tgcccggtg ggtgacccgaa ggatgcagag catgatgcag 540
catctggctc agggcaggac caccgtggtt gtggtcttct ctaaccggca cctggctaga
gtgttcttca ggtccgtggt gctggccaaac ctgactggca aagtgtgggt cgcctcagaa 600
gactggggca tctccacgta catcaccagc gtgactggta tccaaggcat tgggacgggt
ctcggtgtgg ccgtccagca gagacaagtc cctgggctga aggagttga ggagtcttat 660
gtcagggctg taacagctgc tcccagcgct tgcccgagg ggtcctgggt cagcactaac
cagctgtgcc gggagtgcca cacgttccacg actcgtaaca tgccacgct tggagccttc
tccatgagtg ccgcctacag agtgtatgag gctgtgtacg ctgtggccca cggcctccac
cagctccctgg gatgtacttc tgagatctgt tccagaggcc cagtcatacc ctggcagctt
cttcagcaga tctacaaggt gaattttctt ctacatgaga atactgtggc atttgatgac
aacggggaca ctcttaggtta ctacgacatc atcgccctggg actggaaatgg acctgaatgg
acctttgaga tcattggctc tgccctcaactg tctccagttc atctggacat aaataagaca
aaaatccagt ggcacgggaa gaacaatcag gtgcctgtgt cagtggtac cacggactgt
ctggcaggc accacagggt gggtgtgggt tcccaccact gctgtttga gtgtgtgccc 1560

MON-0301.ST25.txt

| | |
|---|------|
| tgcgaaagctg ggacctttct caacatgagt ga ^g c ^t tcaca tctgccagcc ttgtggaaaca | 1620 |
| gaagaatggg caccaagg ^a g ^a gcactact tgcttcccac gcacggtgga gttcttggct | 1680 |
| tggcatgaac ccatctcttt ggtgctaata gcagctaaca cgctattgct gctgctgctg | 1740 |
| gttgggactg ctggcctgtt tgcc ^t ggcat tttcacacac ctgttagtgag gtcagctggg | 1800 |
| ggtaggctgt gcttcctcat gctgggttcc ctgg ^t ggccg gaagttgcag cttctatagc | 1860 |
| tttctcgggg agcccacgg ^t gcccgcgtgc ttgctgcgtc agcccctt ttctctcggg | 1920 |
| tttgccatct tcctctcctg cctgacaatc cgctccttcc aactggtcat catcttcaag | 1980 |
| ttttctacca aggtgcccac attctaccgt acctgggccc aaaaccatgg tg ^c aggtcta | 2040 |
| ttcgtcattg t ^c agctccac ggtccatttgc ctcatctgtc tcacatggct tgtaatgtgg | 2100 |
| accccacgac ccaccagg ^a ataccagcgc ttccccatc tgg ^t gattct cgagtgcaca | 2160 |
| gaggtcaact ctgtaggctt cctgttg ^t g ^t ttcacccaca acattctcct ctccatcagt | 2220 |
| ac ^t tcgtct gcagctac ^t gggtaaggaa ctgcccagaga actataatga agccaaatgt | 2280 |
| gtcac ^t tca gcctgctcct caacttcgt ^t ta tcc ^t ggatcg cttctt ^t cac catggccagc | 2340 |
| at ^t taccagg gcagctac ^t gcctgcggc ^t aatgtgctgg cagg ^t g ^t gac cacactgagc | 2400 |
| ggcggcttca gcggttactt cctccccaa ^t g tgctatgtga ttctctgccc ^t tccagaactc | 2460 |
| aacaatacag aacactttca ggcctccatc caggactaca cgaggcgctg cggcactacc | 2520 |

<210> 8
<211> 2526
<212> DNA
<213> Homo sapiens

| | |
|--|-----|
| <400> 8 atgctgctct gcacggctcg cctgg ^t cg ^t gc ctgcagcttc tcatttctg ctgtgggccc | 60 |
| tttgcc ^t g ^t cc atagcacgga gtcttctcct gacttcaccc tccccggaga ttacctcctg | 120 |
| gcaggcctgt tcc ^t ctc ^t cca ttctggctgt ctgcaggtga ggcacagacc cgaggtgacc | 180 |
| ctgtgtgaca ggtctt ^t g ^t tag cttaatgag catggctacc ac ^t cttcc ^t ca ggctatgcgg | 240 |
| cttggggttg aggagataaa caactccacg gccctgctgc ccaacatcac cctggggtac | 300 |
| cagctgtatg atgtgtgttc tgactctg ^t cc aatgtgtatg ccacgctgag agtgc ^t ctcc | 360 |
| ctgcccagg ^t gc aacaccacat agagctccaa ggagac ^t tc tccactattc ccctacggtg | 420 |
| ctggcagtga ttgggcctga cagcaccaac cgtgctg ^t cc ^t ccacagccgc cctgctgagc | 480 |
| cctttctgg tgcccatgat tagctatg ^t cg g ^t ccagcagcg agacgctc ^t g cgtgaagcgg | 540 |
| cagtatccct ctttctc ^t gc ^t caccatcccc aatgacaagt accaggtgga gaccatgg ^t g | 600 |
| ctgctgctgc agaagttcgg gtggac ^t tg ^t atctctctgg ttggcagcag tgacgactat | 660 |
| ggcagctag ggg ^t g ^t cagg ^t g ^t actggagaac caggccactg gtcagggat ctgcattgct | 720 |
| ttcaaggaca t ^t c ^t atgc ^t cc ^t t ^t c ^t gc ^t cc ^t ag gtgg ^t g ^t gatg agaggatgca gtgc ^t ctcatg | 780 |
| cgccac ^t ctgg cccaggccgg g ^t ccacccg ^t tc ^t g ^t gg ^t tg ^t ttt tttccagccg g ^t c ^t gtggcc | 840 |
| agggtgtttt t ^t c ^t g ^t atccgt g ^t g ^t c ^t g ^t acc aac ^t ctgactg g ^t c ^t agg ^t gtg g ^t tcgc ^t ctca | 900 |

MON-0301.ST25.txt

| | |
|---|------|
| gaag | 960 |
| ggctgggtccatcgatgcatacgttttgggtgcccggatccagcgcat | 960 |
| gtgctggcg tggccatcca gaagaggcgt gtcctggcc tgaaggcg | 1020 |
| tgaagaagccatgcggc cagacaagaa ggcccctagg cttgccaca agggctcctg gtgcagc | 1080 |
| aatcagctct gcagagaatg ccaagtttc atggcacaca cgatgccaa gctcaaagcc | 1140 |
| ttctccatga gttctgccta caacgcatac cggctgtgt atgcggg | 1200 |
| ccatggcctccaccagctcc tggctgtgc ctctggagct tttccaggg gccgagtcta cccctggcag | 1260 |
| cttttggagc agatccacaa ggtgcatttc ttctcacaca aggacactgt ggcttaat | 1320 |
| gacaacagag atcccctcag tagctataac ataattgcct gggactggaa tggacccaag | 1380 |
| tggacccatca cggtcctcgg ttccctccaca tggctccag ttca | 1440 |
| gactaaaatcc agtggcacgg aaaggacaac caggtgccta agtctgtgt ttccagc | 1500 |
| tgtcttgaag ggcaccagcg agtggttacg gtttccatc actgtgtct tgagtgtgt | 1560 |
| ccctgtgggg ctgggacctt cctcaacaag agtgacctt acagatgcca gccttgtgg | 1620 |
| aaagaagagt gggcacctga gggaaagccag acctgcttccgcactgt ggttttttgc | 1680 |
| gttttgcgtg agcacacccctt tgggtgtgt ctggcagcta acacgctgt gctgtgt | 1740 |
| ctgcttggga ctgctggcctt gtttgcctgg cacctagaca cccctgtgtt gaggtcagca | 1800 |
| ggggggccgc ttttatc tatgctggc tccctggcag caggttagtgg cagccttat | 1860 |
| ggcttcttttgc gggaaaccac aaggcctgcg tgcttgcatac gccaggccctt cttgc | 1920 |
| tttgcacca tttccctgtc ctgcctgaca gtcgctcat tccaactaat catcatcttc | 1980 |
| aagtttcca ccaaggta tacattctac cacgcctggg tccaaaacca cggtgctggc | 2040 |
| ctgtttgtga tgatcagctc agcggccctt ctgcattatct gtctaacttg gctgggtgt | 2100 |
| tggacccac tgcctgttag ggaataccag cgttcccccc atctggtgat gcttgagtgc | 2160 |
| acagagacca actccctggg cttcatactg gccttccctt acaatggcct ccttccatc | 2220 |
| agtgcctttgc cctgcagcta cctggtaag gacttgccag agaactacaa cgaggccaaa | 2280 |
| tgtgtcacct tcagcctgctt cttcaacttc gtgtcctggat caccacggcc | 2340 |
| agcgtctacg acggcaagta cctgcctgcg gccaacatga tggctggct gagcagcctg | 2400 |
| agcagcggct tcgggtggta ttttctgcct aagtgcatacg tgatcctctg ccgcccagac | 2460 |
| ctcaacagca cagagcactt ccaggcctcc attcaggact acacgaggcg ctgcggctcc | 2520 |
| acctga | 2526 |

<210> 9
<211> 2577
<212> DNA
<213> Mus musculus

<400> 9
atgccagctt tggctatcat gggctcagc ctggctgctt tcctggagct tggatgggg 60
gcctctttgt gtctgtcaca gcaattcaag gcacaagggg actacatact gggcgggcta 120
tttccctgg gctcaaccga ggaggccact ctcaaccaga gaacacaacc caacagcatc 180
ccgtgcaaca ggttctcacc cttggtttgc ttccctggcca tggctatgaa gatggctgtg 240

MON-0301.ST25.txt

| | |
|--|------|
| gaggagatca acaatggatc tgccttgctc cctgggctgc ggctgggcta tgacctattt | 300 |
| gacacatgct ccgagccagt ggtcaccatg aaatccagtc tcatagttcct ggccaagggtg | 360 |
| ggcagtcaaa gcattgctgc ctactgcaac tacacacagt accaaccgg tgtgctggct | 420 |
| gtcatcgccc cccactcatac agagcttgcc ctcattacag gcaagttctt cagcttcttc | 480 |
| ctcatgccac aggtcagcta tagtgcgcagc atggatcgcc taagtgaccg ggaaacgttt | 540 |
| ccatccttct tccgcacagt gcccagtgc cgggtgcagc tgcaggcagt tgtgactctg | 600 |
| ttgcagaact tcagctggaa ctgggtggcc gccttaggga gtgatgatga ctatggccgg | 660 |
| gaaggctctga gcatcttttc tagtctggcc aatgcacgag gtatctgcat cgcacatgag | 720 |
| ggcctgggtgc cacaacatgca cactagtggc caacagttgg gcaagggtgct ggatgtacta | 780 |
| cgc当地准 accaaagtaa agtacaagtgc ttgggtgcgt ttgcctctgc ccgtgcgtc | 840 |
| tactcccttt ttagttacag catccatcat ggccctctca ccaaggatgt ggtggccagt | 900 |
| gagtcttggc tgacatctgca cctggctcatg acacttccca atattgcccgttgtggcact | 960 |
| gtgcttgggt ttttgcagcg gggtgcctta ctgcctgaat tttccattatgttggagact | 1020 |
| caccttggccc tggccgctga cccagcatc tgcctctca tgaatgcgga gttggatctg | 1080 |
| gaggaacatg tgatggggca acgctgtcca cgggtgtacg acatcatgct gcagaaccta | 1140 |
| tcatctggc tggcagaa cctatcagct gggcaattgc accaccaaatttgcacc | 1200 |
| tatgcagctg tgcactgtgt ggctcaagcc ctccacaaca ccctacagtg caatgtctca | 1260 |
| cattgccacg tatcagaaca tggcacttaccc tggcagctcc tggagaacat gtacaatatg | 1320 |
| agtttccatg ctcgagactt gacactacag tttgatgtgc aagggaaatgt agacatggaa | 1380 |
| tatgacactga agatgtgggt gtggcagagc cctacacactg tattacatac tgtggcacc | 1440 |
| ttcaacggca cccttcagct gcagcagtct aaaatgtact ggccaggcaa ccaggtgcct | 1500 |
| gtctcccaact gttcccgcca gtgc当地准 gcccagggttc gccgagtaaa gggctttcat | 1560 |
| tcctgctgct atgactgcgt ggactgc当地准 gccccagct accggaagca tccagatgac | 1620 |
| ttcacctgta ctccatgtaa ccaggaccag tggcccccag agaaaagcac agcctgctta | 1680 |
| cctcgcaggc ccaagttct ggcttgggg gagccagtt tgctgtcaact cctcctgctg | 1740 |
| cattgcctgg tgctgggtct agcactggct gctctgggc tctctgtcca ccactggac | 1800 |
| agccctcttg tccaggccctc aggtggctca cagttctgct ttggcctgat ctgccttaggc | 1860 |
| ctcttcgtcc tcagttgtccct tctgttccca gggcggccaa gctctgc当地准 ctgccttgca | 1920 |
| caacaaccaa tggctcacct ccctctcaca ggctgcctga gcacactt cctgcaagca | 1980 |
| gctgagacct ttgtggagtc tgagctgc当地准 ctgagctggg caaaactggct atgcagctac | 2040 |
| cttcggggac tctgggcctg gctagttggta ctgttggccca cttttgtggaa ggcagcacta | 2100 |
| tgtgcctggat atttgcgtcc tttccacca gaggtgggtga cagactggc agtgc当地准 | 2160 |
| acagaggtac tggagcactg ccacgtgcgt tcctgggtca gcctgggctt ggtgc当地准 | 2220 |
| accaatgcaa tggtagcttt cctctgcttt ctgggcactt tcctggtaca gagccagcct | 2280 |
| ggccgctaca accgtgcccgg tggcttcacc ttgc当地准 tagtttattt catcacctgg | 2340 |

MON-0301.ST25.txt

```

gtctctttg tgcccctcct ggccaatgtg caggtggcct accagccagc tgtgcagatg 2400
ggtgctatcc tagtctgtgc cctgggcac tccacacct caagtgttat 2460
gtgcttctt ggctgccaata gctcaacacc caggagttct tcctggaaag gaatgccaag 2520
aaagcagcag atgagaacag tggcggtggt gagggcagctc agggacacaa tgaatga 2577

```

<210> 10
<211> 2577
<212> DNA
<213> *Rattus rattus*

<400> 10
atgccgggtt tggctatctt gggcctcagt ctggctgctt tcctggagct tggatgggg 60
tcctttgt gtctgtcaca gcaattcaag gcacaagggg actatatatt gggtggacta 120
tttccccctgg gcacaactga ggaggccact ctcaaccaga gaacacagcc caacggcatc 180
ctatgtacca gttctcgcc ccttggtttg ttccctggcca tggctatgaa gatggctgta 240
gaggagatca acaatggatc tgccctgctc cctgggctgc gactgggcta tgacctgtt 300
gacacatgct cagagccagt ggtcaccatg aagcccagcc tcatgttcat ggccaagggtg 360
ggaagtcaaa gcattgctgc ctactgcaac tacacacagt accaaccggc tgtgtggct 420
gtcattggtc cccactcatc agagcttgc ctcattacag gcaagttctt cagcttcttc 480
ctcatgccac aggtcagcta tagtgccagc atggatcgcc taagtgaccg ggaaacattt 540
ccatccttct tccgcacagt gcccagtgc acgggtgcagc tgcaggccgt tgtgacactg 600
ttgcagaatt tcagctggaa ctgggtggct gccttaggtt gtgatgtatca ctatggccgg 660
gaaggtctga gcatactttc tggcttgcc aactcacagag gtatctgat tgcacacagag 720
ggcctggtgc cacaacatga cactagtggc caacaattgg gcaagggtggt ggatgtgcta 780
cgccaaagtga accaaagcaa agtacagggtg gtggtgctgt ttgcattctgc ccgtgctgtc 840
tactcccttt ttagctacag catccttcattt gacctctcac ccaaggtatg ggtggccagt 900
gagtcctggc tgacctctga cctggtcattt acacttccca atattgcccgttgtggcact 960
gttcttgggt ttctgcagcg cggtgcccta ctgcctgaat ttcccattt tgtggagact 1020
cgccctggccc tagctgctga cccaaacattt tgcctccccc tgaaagctga gttggatctg 1080
gaggagcgcg tgatggggcc acgctgtca caatgtgact acatcatgct acagaacctg 1140
tcatactggc tgatgcagaa cctatcagct gggcagttgc accaccaaattt tttgcaacc 1200
tatgcagctg tgtacagtgt ggctcaggcc cttcacaaca ccctgcagtg caatgtctca 1260
cattgccaca catcagagcc tggcaaccc tggcagctcc tggagaacat gtacaatatg 1320
agtttccgtg ctcgagactt gacactgcag tttgatgcca aaggaggtgt agacatggaa 1380
tatgacctga agatgtgggt gtggcagagc cttcacaactt tactacatc tgcggccacc 1440
ttcaacggca cccttcagct gcagcactcg aaaatgtatt ggccaggccaa ccaggtgcca 1500
gtctcccaagt gctccggca gtgcaaagat ggccagggtgc gcagagtaaa gggctttcat 1560
tcctactgtatqactgtgt qqactqcaaq qcaggggagct accggaaagca tccagatgac 1620

MON-0301.ST25.txt

| | | | | | | |
|------------|--------------|-------------|-------------|-------------|-------------|------|
| ttcacctgta | ctccatgtgg | caaggatcag | tggccccag | aaaaaaagcac | aacctgctta | 1680 |
| cctcgaggc | ccaagtttct | ggcttggggg | gagccagctg | tgtgtcact | tctctgctg | 1740 |
| ctttgcctgg | tgctggcct | gacactggct | gccctggggc | tcttgcctca | ctactggac | 1800 |
| agccctcttg | ttcaggcctc | aggtgggtca | ctgttctgct | ttggcctgat | ctgccttaggc | 1860 |
| ctcttctgcc | tcagtgtcct | tctgttccc | ggacgaccac | gctctgccag | ctgccttgcc | 1920 |
| caacaaccaa | tggctcacct | ccctctcaca | ggctgcctga | gcacactctt | cctgcaagca | 1980 |
| gccgagatct | tttgtggagtc | ttagctgcca | ctgagttggg | caaactggct | ctgcagctac | 2040 |
| cttcggggcc | cctgggcttg | gctgggtga | ctgctggcca | ctcttgcgga | ggctgcacta | 2100 |
| tgtgcctggt | acttgcattggc | tttccctcca | gaggtgggtga | cagattggca | ggtgctgccc | 2160 |
| acggaggtac | tggaacactg | ccgcatgcgt | tcctgggtca | gcctgggctt | ggtgacatc | 2220 |
| accaatgcag | tgttagcttt | cctctgcctt | ctgggcactt | tcctggtaca | gagccagcct | 2280 |
| ggtcgctata | accgtgcccc | tggcctcacc | ttcgccatgc | tagtttattt | catcatctgg | 2340 |
| gtctcttttg | tgcgcctcct | ggctaattgt | caggtggcct | accagccagc | tgtgcagatg | 2400 |
| ggtgctatct | tattctgtgc | cctgggcattc | ctggccacct | tccacctgcc | caaatgctat | 2460 |
| gtacttctgt | ggctgccaga | gctcaacacc | caggagttct | tcctgggaag | gagccccaaag | 2520 |
| gaagcatcag | atggaatag | tggtagtagt | gaggcaactc | ggggacacag | tgaatga | 2577 |

<210> 11
<211> 2559
<212> DNA
<213> Homo sapiens

| | | | | | | | |
|----------|-------------|-------------|-------------|-------------|------------|-------------|-----|
| <400> 11 | atgctgggcc | ctgctgtcct | gggcctcagc | ctctggcctc | tcctgcaccc | tgggacgggg | 60 |
| | gccccattgt | gcctgtcaca | gcaacttagg | atgaaggggg | actacgtct | ggggggggctg | 120 |
| | ttccccctgg | gcgaggccga | ggaggctggc | ctccgcagcc | ggacacggcc | cagcagccct | 180 |
| | gtgtgcacca | ggttctccct | aaacggctg | ctctggcac | tggccatgaa | aatggccgt | 240 |
| | gaggagatca | acaacaagtc | ggatctgt | cccggtctgc | gcctggct | cgacctttt | 300 |
| | gatacgtct | cggagccctgt | ggtggccatg | aagccccagcc | tcatgttct | ggccaaggca | 360 |
| | ggcagccgcg | acatcgccgc | ctactgcaac | tacacgcagt | accagcccc | tgtgtggct | 420 |
| | gtcatcgggc | cccaactcg | agagctcgcc | atggtcaccc | gcaagttctt | cagttcttc | 480 |
| | ctcatgcccc | aggtcagcta | cggtgctagc | atggagctc | tgagcgcccc | ggagaccttc | 540 |
| | ccctccttct | tccgcaccgt | gcccagcgc | cgtgtgcagc | tgacggccgc | cgggagctg | 600 |
| | ctgcaggagt | tccgcggaa | ctgggtggcc | gccctggca | gcgacgacga | gtacggccgg | 660 |
| | cagggcctga | gcatcttctc | ggccctggcc | gccccacgc | gcatctgc | cgccacgag | 720 |
| | ggcctgggtgc | cgctgcccc | tgccgatgac | tgcggctgg | ggaagggtca | ggacgtcctg | 780 |
| | caccaggtga | accagagcag | cgtgcaggt | gtgtgtctgt | tgcctccgt | gcacgcccgc | 840 |
| | cacgcctct | tcaactacag | catcagcagc | aggctctcgc | ccaagggtgt | ggtggccagc | 900 |
| | gaggcctggc | tgacctctga | cctggctcatg | gggctgcccc | gcatggccca | gatgggcac | 960 |

MON-0301.ST25.txt

| | |
|--|------|
| gtgcttggct tcctccagag ggggccag ctgcacgagt tccccagta cgtgaagacg | 1020 |
| cacctggccc tggccaccga cccggccttc tgctctgccc tggcgagag ggagcagggt | 1080 |
| ctggaggagg acgtggtggg ccagcgtgc ccgcagtgtg actgcacac gctcagaac | 1140 |
| gtgagcgcag ggctaaatca ccaccagac ttctctgtct acgcagctgt gtatagcgtg | 1200 |
| gcccaggccc tgcacaacac tttcagtgc aacgcctcag gctgccccgc gcaggacccc | 1260 |
| gtgaagccct ggcagctcct ggagaacatg tacaacctga cttccacgt gggcggctg | 1320 |
| ccgctgcggt tcgacagcag cgaaaacgtg gacatggagt acgacactgaa gctgtgggtg | 1380 |
| tggcagggct cagtgcctcag gctccacgac gtggcaggt tcaacggcag cctcaggaca | 1440 |
| gagcgcctga agatccgctg gcacacgtct gacaaccaga agcccggtc ccggctcg | 1500 |
| cggcagtgcc aggagggcca ggtgcgcgg gtcaagggtt tccactcctg ctgctacgac | 1560 |
| tgtgtggact gcgaggcggg cagctaccgg caaaacccag acgacatcgc ctgcacctt | 1620 |
| tgtggccagg atgagtggtc cccggagcga agcacacgct gttccgcgg caggtctcgg | 1680 |
| ttcctggcat gggcgagcc ggctgtgtc ctgctgctcc tgctgctgag cttggcgtcg | 1740 |
| ggccttgtgc tggctgcttt gggctgttc gttcaccatc gggacagccc actggttcag | 1800 |
| gcctcggggg ggccctggc ctgcttggc ctgggtgtgcc tggcctggt ctgcctcagc | 1860 |
| gtcctctgt tccctggcca gcccagccct gcccgtatgcc tggcccgacca gcccgtgtcc | 1920 |
| caccccccgc tcacggcgtc cctgagcaca ctcttcgtc aggcggccga gatcttcgt | 1980 |
| gagtcaaac tgcctctgag ctggcagac cgctgagtg gctgcctgcg gggccctgg | 2040 |
| gcctggctgg tggctgtcgt ggcattgtcgt gtggagggtcg cactgtgcac ctggtaacctg | 2100 |
| gtggccttcc cgccggaggt ggtgacggac tggcacatgc tgcccacgga ggcgtgggt | 2160 |
| cactgccgca cacgctcctg ggtcagcttc ggcctagcgc acgccaccaa tgccacgctg | 2220 |
| gccttcgtcgtt gttccctggg cactttcctg gtgcggagcc agccggcccg ctacaaccgt | 2280 |
| gcccgtggcc tcacctttgc catgctggcc tacttcatca cttgggtctc ctttgtgcc | 2340 |
| ctcctggcca atgtgcagg ggtcctcagg cccggcgtc agatggcgc cctcctgctc | 2400 |
| tgtgtctgg gcatcctggc tgccttccac ctgcccagggt gttacctgct catgcccag | 2460 |
| ccaggcgtca acaccccccga gttcttcctg ggagggggcc ctggggatgc ccaaggccag | 2520 |
| aatgacggga acacaggaaa tcagggaaa catgagtga | 2559 |

<210> 12
<211> 852
<212> PRT
<213> Homo sapiens

<400> 12

| | | | |
|---|---|----|----|
| Met Leu Gly Pro Ala Val Leu Gly Leu Ser Leu Trp Ala Leu Leu His | | | |
| 1 | 5 | 10 | 15 |

| | | |
|---|----|----|
| Pro Gly Thr Gly Ala Pro Leu Cys Leu Ser Gln Gln Leu Arg Met Lys | | |
| 20 | 25 | 30 |

MON-0301.ST25.txt

Gly Asp Tyr Val Leu Gly Gly Leu Phe Pro Leu Gly Glu Ala Glu Glu
35 40 45

Ala Gly Leu Arg Ser Arg Thr Arg Pro Ser Ser Pro Val Cys Thr Arg
50 55 60

Phe Ser Ser Asn Gly Leu Leu Trp Ala Leu Ala Met Lys Met Ala Val
65 70 75 80

Glu Glu Ile Asn Asn Lys Ser Asp Leu Leu Pro Gly Leu Arg Leu Gly
85 90 95

Tyr Asp Leu Phe Asp Thr Cys Ser Glu Pro Val Val Ala Met Lys Pro
100 105 110

Ser Leu Met Phe Leu Ala Lys Ala Gly Ser Arg Asp Ile Ala Ala Tyr
115 120 125

Cys Asn Tyr Thr Gln Tyr Gln Pro Arg Val Leu Ala Val Ile Gly Pro
130 135 140

His Ser Ser Glu Leu Ala Met Val Thr Gly Lys Phe Phe Ser Phe Phe
145 150 155 160

Leu Met Pro Gln Val Ser Tyr Gly Ala Ser Met Glu Leu Leu Ser Ala
165 170 175

Arg Glu Thr Phe Pro Ser Phe Phe Arg Thr Val Pro Ser Asp Arg Val
180 185 190

Gln Leu Thr Ala Ala Ala Glu Leu Leu Gln Glu Phe Gly Trp Asn Trp
195 200 205

Val Ala Ala Leu Gly Ser Asp Asp Glu Tyr Gly Arg Gln Gly Leu Ser
210 215 220

Ile Phe Ser Ala Leu Ala Ala Arg Gly Ile Cys Ile Ala His Glu
225 230 235 240

Gly Leu Val Pro Leu Pro Arg Ala Asp Asp Ser Arg Leu Gly Lys Val
245 250 255

Gln Asp Val Leu His Gln Val Asn Gln Ser Ser Val Gln Val Val Leu
260 265 270

Leu Phe Ala Ser Val His Ala Ala His Ala Leu Phe Asn Tyr Ser Ile
275 280 285

Ser Ser Arg Leu Ser Pro Lys Val Trp Val Ala Ser Glu Ala Trp Leu
290 295 300

Thr Ser Asp Leu Val Met Gly Leu Pro Gly Met Ala Gln Met Gly Thr

MON-0301.ST25.txt
 305 310 315 320
 Val Leu Gly Phe Leu Gln Arg Gly Ala Gln Leu His Glu Phe Pro Gln
 325 330 335
 Tyr Val Lys Thr His Leu Ala Leu Ala Thr Asp Pro Ala Phe Cys Ser
 340 345 350
 Ala Leu Gly Glu Arg Glu Gln Gly Leu Glu Glu Asp Val Val Gly Gln
 355 360 365
 Arg Cys Pro Gln Cys Asp Cys Ile Thr Leu Gln Asn Val Ser Ala Gly
 370 375 380
 Leu Asn His His Gln Thr Phe Ser Val Tyr Ala Ala Val Tyr Ser Val
 385 390 395 400
 Ala Gln Ala Leu His Asn Thr Leu Gln Cys Asn Ala Ser Gly Cys Pro
 405 410 415
 Ala Gln Asp Pro Val Lys Pro Trp Gln Leu Leu Glu Asn Met Tyr Asn
 420 425 430
 Leu Thr Phe His Val Gly Gly Leu Pro Leu Arg Phe Asp Ser Ser Gly
 435 440 445
 Asn Val Asp Met Glu Tyr Asp Leu Lys Leu Trp Val Trp Gln Gly Ser
 450 455 460
 Val Pro Arg Leu His Asp Val Gly Arg Phe Asn Gly Ser Leu Arg Thr
 465 470 475 480
 Glu Arg Leu Lys Ile Arg Trp His Thr Ser Asp Asn Gln Lys Pro Val
 485 490 495
 Ser Arg Cys Ser Arg Gln Cys Gln Glu Gly Gln Val Arg Arg Val Lys
 500 505 510
 Gly Phe His Ser Cys Cys Tyr Asp Cys Val Asp Cys Glu Ala Gly Ser
 515 520 525
 Tyr Arg Gln Asn Pro Asp Asp Ile Ala Cys Thr Phe Cys Gly Gln Asp
 530 535 540
 Glu Trp Ser Pro Glu Arg Ser Thr Arg Cys Phe Arg Arg Arg Ser Arg
 545 550 555 560
 Phe Leu Ala Trp Gly Glu Pro Ala Val Leu Leu Leu Leu Leu Leu
 565 570 575
 Ser Leu Ala Leu Gly Leu Val Leu Ala Ala Leu Gly Leu Phe Val His

MON-0301.ST25.txt

His Arg Asp Ser Pro Leu Val Gln Ala Ser Gly Gly Pro Leu Ala Cys
595 600 605

Phe Gly Leu Val Cys Leu Gly Leu Val Cys Leu Ser Val Leu Leu Phe
610 615 620

Pro Gly Gln Pro Ser Pro Ala Arg Cys Leu Ala Gln Gln Pro Leu Ser
625 630 635 640

His Leu Pro Leu Thr Gly Cys Leu Ser Thr Leu Phe Leu Gln Ala Ala
645 650 655

Glu Ile Phe Val Glu Ser Glu Leu Pro Leu Ser Trp Ala Asp Arg Leu
660 665 670

Ser Gly Cys Leu Arg Gly Pro Trp Ala Trp Leu Val Val Leu Leu Ala
675 680 685

Met Leu Val Glu Val Ala Leu Cys Thr Trp Tyr Leu Val Ala Phe Pro
690 695 700

Pro Glu Val Val Thr Asp Trp His Met Leu Pro Thr Glu Ala Leu Val
705 710 715 720

His Cys Arg Thr Arg Ser Trp Val Ser Phe Gly Leu Ala His Ala Thr
725 730 735

Asn Ala Thr Leu Ala Phe Leu Cys Phe Leu Gly Thr Phe Leu Val Arg
740 745 750

Ser Gln Pro Gly Arg Tyr Asn Arg Ala Arg Gly Leu Thr Phe Ala Met
755 760 765

Leu Ala Tyr Phe Ile Thr Trp Val Ser Phe Val Pro Leu Leu Ala Asn
770 775 780

Val Gln Val Val Leu Arg Pro Ala Val Gln Met Gly Ala Leu Leu Leu
785 790 795 800

Cys Val Leu Gly Ile Leu Ala Ala Phe His Leu Pro Arg Cys Tyr Leu
805 810 815

Leu Met Arg Gln Pro Gly Leu Asn Thr Pro Glu Phe Phe Leu Gly Gly
820 825 830

Gly Pro Gly Asp Ala Gln Gly Gln Asn Asp Gly Asn Thr Gly Asn Gln
835 840 845

Gly Lys His Glu
850

MON-0301.ST25.txt

<211> 858

<212> PRT

<213> Mus musculus

<400> 13

Met Pro Ala Leu Ala Ile Met Gly Leu Ser Leu Ala Ala Phe Leu Glu
1 5 10 15

Leu Gly Met Gly Ala Ser Leu Cys Leu Ser Gln Gln Phe Lys Ala Gln
20 25 30

Gly Asp Tyr Ile Leu Gly Gly Leu Phe Pro Leu Gly Ser Thr Glu Glu
35 40 45

Ala Thr Leu Asn Gln Arg Thr Gln Pro Asn Ser Ile Pro Cys Asn Arg
50 55 60

Phe Ser Pro Leu Gly Leu Phe Leu Ala Met Ala Met Lys Met Ala Val
65 70 75 80

Glu Glu Ile Asn Asn Gly Ser Ala Leu Leu Pro Gly Leu Arg Leu Gly
85 90 95

Tyr Asp Leu Phe Asp Thr Cys Ser Glu Pro Val Val Thr Met Lys Ser
100 105 110

Ser Leu Met Phe Leu Ala Lys Val Gly Ser Gln Ser Ile Ala Ala Tyr
115 120 125

Cys Asn Tyr Thr Gln Tyr Gln Pro Arg Val Leu Ala Val Ile Gly Pro
130 135 140

His Ser Ser Glu Leu Ala Leu Ile Thr Gly Lys Phe Phe Ser Phe Phe
145 150 155 160

Leu Met Pro Gln Val Ser Tyr Ser Ala Ser Met Asp Arg Leu Ser Asp
165 170 175

Arg Glu Thr Phe Pro Ser Phe Phe Arg Thr Val Pro Ser Asp Arg Val
180 185 190

Gln Leu Gln Ala Val Val Thr Leu Leu Gln Asn Phe Ser Trp Asn Trp
195 200 205

Val Ala Ala Leu Gly Ser Asp Asp Tyr Gly Arg Glu Gly Leu Ser
210 215 220

Ile Phe Ser Ser Leu Ala Asn Ala Arg Gly Ile Cys Ile Ala His Glu
225 230 235 240

Gly Leu Val Pro Gln His Asp Thr Ser Gly Gln Gln Leu Gly Lys Val
245 250 255

MON-0301.ST25.txt

Leu Asp Val Leu Arg Gln Val Asn Gln Ser Lys Val Gln Val Val Val
260 265 270

Leu Phe Ala Ser Ala Arg Ala Val Tyr Ser Leu Phe Ser Tyr Ser Ile
275 280 285

His His Gly Leu Ser Pro Lys Val Trp Val Ala Ser Glu Ser Trp Leu
290 295 300

Thr Ser Asp Leu Val Met Thr Leu Pro Asn Ile Ala Arg Val Gly Thr
305 310 315 320

Val Leu Gly Phe Leu Gln Arg Gly Ala Leu Leu Pro Glu Phe Ser His
325 330 335

Tyr Val Glu Thr His Leu Ala Leu Ala Asp Pro Ala Phe Cys Ala
340 345 350

Ser Leu Asn Ala Glu Leu Asp Leu Glu Glu His Val Met Gly Gln Arg
355 360 365

Cys Pro Arg Cys Asp Asp Ile Met Leu Gln Asn Leu Ser Ser Gly Leu
370 375 380

Leu Gln Asn Leu Ser Ala Gly Gln Leu His His Gln Ile Phe Ala Thr
385 390 395 400

Tyr Ala Ala Val Tyr Ser Val Ala Gln Ala Leu His Asn Thr Leu Gln
405 410 415

Cys Asn Val Ser His Cys His Val Ser Glu His Val Leu Pro Trp Gln
420 425 430

Leu Leu Glu Asn Met Tyr Asn Met Ser Phe His Ala Arg Asp Leu Thr
435 440 445

Leu Gln Phe Asp Ala Glu Gly Asn Val Asp Met Glu Tyr Asp Leu Lys
450 455 460

Met Trp Val Trp Gln Ser Pro Thr Pro Val Leu His Thr Val Gly Thr
465 470 475 480

Phe Asn Gly Thr Leu Gln Leu Gln Ser Lys Met Tyr Trp Pro Gly
485 490 495

Asn Gln Val Pro Val Ser Gln Cys Ser Arg Gln Cys Lys Asp Gly Gln
500 505 510

Val Arg Arg Val Lys Gly Phe His Ser Cys Cys Tyr Asp Cys Val Asp
515 520 525

Cys Lys Ala Gly Ser Tyr Arg Lys His Pro Asp Asp Phe Thr Cys Thr
530 535 540

MON-0301.ST25.txt

Pro Cys Asn Gln Asp Gln Trp Ser Pro Glu Lys Ser Thr Ala Cys Leu
545 550 555 560

Pro Arg Arg Pro Lys Phe Leu Ala Trp Gly Glu Pro Val Val Leu Ser
565 570 575

Leu Leu Leu Leu Cys Leu Val Leu Gly Leu Ala Leu Ala Ala Leu
580 585 590

Gly Leu Ser Val His His Trp Asp Ser Pro Leu Val Gln Ala Ser Gly
595 600 605

Gly Ser Gln Phe Cys Phe Gly Leu Ile Cys Leu Gly Leu Phe Cys Leu
610 615 620

Ser Val Leu Leu Phe Pro Gly Arg Pro Ser Ser Ala Ser Cys Leu Ala
625 630 635 640

Gln Gln Pro Met Ala His Leu Pro Leu Thr Gly Cys Leu Ser Thr Leu
645 650 655

Phe Leu Gln Ala Ala Glu Thr Phe Val Glu Ser Glu Leu Pro Leu Ser
660 665 670

Trp Ala Asn Trp Leu Cys Ser Tyr Leu Arg Gly Leu Trp Ala Trp Leu
675 680 685

Val Val Leu Leu Ala Thr Phe Val Glu Ala Ala Leu Cys Ala Trp Tyr
690 695 700

Leu Ile Ala Phe Pro Pro Glu Val Val Thr Asp Trp Ser Val Leu Pro
705 710 715 720

Thr Glu Val Leu Glu His Cys His Val Arg Ser Trp Val Ser Leu Gly
725 730 735

Leu Val His Ile Thr Asn Ala Met Leu Ala Phe Leu Cys Phe Leu Gly
740 745 750

Thr Phe Leu Val Gln Ser Gln Pro Gly Arg Tyr Asn Arg Ala Arg Gly
755 760 765

Leu Thr Phe Ala Met Leu Ala Tyr Phe Ile Thr Trp Val Ser Phe Val
770 775 780

Pro Leu Leu Ala Asn Val Gln Val Ala Tyr Gln Pro Ala Val Gln Met
785 790 795 800

Gly Ala Ile Leu Val Cys Ala Leu Gly Ile Leu Val Thr Phe His Leu
805 810 815

MON-0301.ST25.txt

Pro Lys Cys Tyr Val Leu Leu Trp Leu Pro Lys Leu Asn Thr Gln Glu
 820 825 830

Phe Phe Leu Gly Arg Asn Ala Lys Lys Ala Ala Asp Glu Asn Ser Gly
 835 840 845

Gly Gly Glu Ala Ala Gln Gly His Asn Glu
 850 855

<210> 14
 <211> 858
 <212> PRT
 <213> Rattus rattus

<400> 14

Met Pro Gly Leu Ala Ile Leu Gly Leu Ser Leu Ala Ala Phe Leu Glu
 1 5 10 15

Leu Gly Met Gly Ser Ser Leu Cys Leu Ser Gln Gln Phe Lys Ala Gln
 20 25 30

Gly Asp Tyr Ile Leu Gly Gly Leu Phe Pro Leu Gly Thr Thr Glu Glu
 35 40 45

Ala Thr Leu Asn Gln Arg Thr Gln Pro Asn Gly Ile Leu Cys Thr Arg
 50 55 60

Phe Ser Pro Leu Gly Leu Phe Leu Ala Met Ala Met Lys Met Ala Val
 65 70 75 80

Glu Glu Ile Asn Asn Gly Ser Ala Leu Pro Gly Leu Arg Leu Gly
 85 90 95

Tyr Asp Leu Phe Asp Thr Cys Ser Glu Pro Val Val Thr Met Lys Pro
 100 105 110

Ser Leu Met Phe Met Ala Lys Val Gly Ser Gln Ser Ile Ala Ala Tyr
 115 120 125

Cys Asn Tyr Thr Gln Tyr Gln Pro Arg Val Leu Ala Val Ile Gly Pro
 130 135 140

His Ser Ser Glu Leu Ala Leu Ile Thr Gly Lys Phe Phe Ser Phe Phe
 145 150 155 160

Leu Met Pro Gln Val Ser Tyr Ser Ala Ser Met Asp Arg Leu Ser Asp
 165 170 175

Arg Glu Thr Phe Pro Ser Phe Phe Arg Thr Val Pro Ser Asp Arg Val
 180 185 190

Gln Leu Gln Ala Val Val Thr Leu Leu Gln Asn Phe Ser Trp Asn Trp
 195 200 205

MON-0301.ST25.txt

Val Ala Ala Leu Gly Ser Asp Asp Asp Tyr Gly Arg Glu Gly Leu Ser
210 215 220

Ile Phe Ser Gly Leu Ala Asn Ser Arg Gly Ile Cys Ile Ala His Glu
225 230 235 240

Gly Leu Val Pro Gln His Asp Thr Ser Gly Gln Gln Leu Gly Lys Val
245 250 255

Val Asp Val Leu Arg Gln Val Asn Gln Ser Lys Val Gln Val Val Val
260 265 270

Leu Phe Ala Ser Ala Arg Ala Val Tyr Ser Leu Phe Ser Tyr Ser Ile
275 280 285

Leu His Asp Leu Ser Pro Lys Val Trp Val Ala Ser Glu Ser Trp Leu
290 295 300

Thr Ser Asp Leu Val Met Thr Leu Pro Asn Ile Ala Arg Val Gly Thr
305 310 315 320

Val Leu Gly Phe Leu Gln Arg Gly Ala Leu Leu Pro Glu Phe Ser His
325 330 335

Tyr Val Glu Thr Arg Leu Ala Leu Ala Ala Asp Pro Thr Phe Cys Ala
340 345 350

Ser Leu Lys Ala Glu Leu Asp Leu Glu Glu Arg Val Met Gly Pro Arg
355 360 365

Cys Ser Gln Cys Asp Tyr Ile Met Leu Gln Asn Leu Ser Ser Gly Leu
370 375 380

Met Gln Asn Leu Ser Ala Gly Gln Leu His His Gln Ile Phe Ala Thr
385 390 395 400

Tyr Ala Ala Val Tyr Ser Val Ala Gln Ala Leu His Asn Thr Leu Gln
405 410 415

Cys Asn Val Ser His Cys His Thr Ser Glu Pro Val Gln Pro Trp Gln
420 425 430

Leu Leu Glu Asn Met Tyr Asn Met Ser Phe Arg Ala Arg Asp Leu Thr
435 440 445

Leu Gln Phe Asp Ala Lys Gly Ser Val Asp Met Glu Tyr Asp Leu Lys
450 455 460

Met Trp Val Trp Gln Ser Pro Thr Pro Val Leu His Thr Val Gly Thr
465 470 475 480

Phe Asn Gly Thr Leu Gln Leu Gln His Ser Lys Met Tyr Trp Pro Gly

485

MON-0301.ST25.txt

490

495

Asn Gln Val Pro Val Ser Gln Cys Ser Arg Gln Cys Lys Asp Gly Gln
500 505 510

Val Arg Arg Val Lys Gly Phe His Ser Cys Cys Tyr Asp Cys Val Asp
515 520 525

Cys Lys Ala Gly Ser Tyr Arg Lys His Pro Asp Asp Phe Thr Cys Thr
530 535 540

Pro Cys Gly Lys Asp Gln Trp Ser Pro Glu Lys Ser Thr Thr Cys Leu
545 550 555 560

Pro Arg Arg Pro Lys Phe Leu Ala Trp Gly Glu Pro Ala Val Leu Ser
565 570 575

Leu Leu Leu Leu Cys Leu Val Leu Gly Leu Thr Leu Ala Ala Leu
580 585 590

Gly Leu Phe Val His Tyr Trp Asp Ser Pro Leu Val Gln Ala Ser Gly
595 600 605

Gly Ser Leu Phe Cys Phe Gly Leu Ile Cys Leu Gly Leu Phe Cys Leu
610 615 620

Ser Val Leu Leu Phe Pro Gly Arg Pro Arg Ser Ala Ser Cys Leu Ala
625 630 635 640

Gln Gln Pro Met Ala His Leu Pro Leu Thr Gly Cys Leu Ser Thr Leu
645 650 655

Phe Leu Gln Ala Ala Glu Ile Phe Val Glu Ser Glu Leu Pro Leu Ser
660 665 670

Trp Ala Asn Trp Leu Cys Ser Tyr Leu Arg Gly Pro Trp Ala Trp Leu
675 680 685

Val Val Leu Leu Ala Thr Leu Val Glu Ala Ala Leu Cys Ala Trp Tyr
690 695 700

Leu Met Ala Phe Pro Pro Glu Val Val Thr Asp Trp Gln Val Leu Pro
705 710 715 720

Thr Glu Val Leu Glu His Cys Arg Met Arg Ser Trp Val Ser Leu Gly
725 730 735

Leu Val His Ile Thr Asn Ala Val Leu Ala Phe Leu Cys Phe Leu Gly
740 745 750

Thr Phe Leu Val Gln Ser Gln Pro Gly Arg Tyr Asn Arg Ala Arg Gly
755 760 765

MON-0301.ST25.txt

Leu Thr Phe Ala Met Leu Ala Tyr Phe Ile Ile Trp Val Ser Phe Val
770 775 780

Pro Leu Leu Ala Asn Val Gln Val Ala Tyr Gln Pro Ala Val Gln Met
785 790 795 800

Gly Ala Ile Leu Phe Cys Ala Leu Gly Ile Leu Ala Thr Phe His Leu
805 810 815

Pro Lys Cys Tyr Val Leu Leu Trp Leu Pro Glu Leu Asn Thr Gln Glu
820 825 830

Phe Phe Leu Gly Arg Ser Pro Lys Glu Ala Ser Asp Gly Asn Ser Gly
835 840 845

Ser Ser Glu Ala Thr Arg Gly His Ser Glu
850 855

<210> 15

<211> 842

<212> PRT

<213> Mus musculus

<400> 15

Met Leu Phe Trp Ala Ala His Leu Leu Leu Ser Leu Gln Leu Ala Val
1 5 10 15

Ala Tyr Cys Trp Ala Phe Ser Cys Gln Arg Thr Glu Ser Ser Pro Gly
20 25 30

Phe Ser Leu Pro Gly Asp Phe Leu Leu Ala Gly Leu Phe Ser Leu His
35 40 45

Ala Asp Cys Leu Gln Val Arg His Arg Pro Leu Val Thr Ser Cys Asp
50 55 60

Arg Ser Asp Ser Phe Asn Gly His Gly Tyr His Leu Phe Gln Ala Met
65 70 75 80

Arg Phe Thr Val Glu Glu Ile Asn Asn Ser Thr Ala Leu Leu Pro Asn
85 90 95

Ile Thr Leu Gly Tyr Glu Leu Tyr Asp Val Cys Ser Glu Ser Ser Asn
100 105 110

Val Tyr Ala Thr Leu Arg Val Leu Ala Gln Gln Gly Thr Gly His Leu
115 120 125

Glu Met Gln Arg Asp Leu Arg Asn His Ser Ser Lys Val Val Ala Leu
130 135 140

Ile Gly Pro Asp Asn Thr Asp His Ala Val Thr Thr Ala Ala Leu Leu
145 150 155 160

MON-0301.ST25.txt

Ser Pro Phe Leu Met Pro Leu Val Ser Tyr Glu Ala Ser Ser Val Ile
165 170 175

Leu Ser Gly Lys Arg Lys Phe Pro Ser Phe Leu Arg Thr Ile Pro Ser
180 185 190

Asp Lys Tyr Gln Val Glu Val Ile Val Arg Leu Leu Gln Ser Phe Gly
195 200 205

Trp Val Trp Ile Ser Leu Val Gly Ser Tyr Gly Asp Tyr Gly Gln Leu
210 215 220

Gly Val Gln Ala Leu Glu Glu Leu Ala Thr Pro Arg Gly Ile Cys Val
225 230 235 240

Ala Phe Lys Asp Val Val Pro Leu Ser Ala Gln Ala Gly Asp Pro Arg
245 250 255

Met Gln Arg Met Met Leu Arg Leu Ala Arg Ala Arg Thr Thr Val Val
260 265 270

Val Val Phe Ser Asn Arg His Leu Ala Gly Val Phe Phe Arg Ser Val
275 280 285

Val Leu Ala Asn Leu Thr Gly Lys Val Trp Ile Ala Ser Glu Asp Trp
290 295 300

Ala Ile Ser Thr Tyr Ile Thr Asn Val Pro Gly Ile Gln Gly Ile Gly
305 310 315 320

Thr Val Leu Gly Val Ala Ile Gln Gln Arg Gln Val Pro Gly Leu Lys
325 330 335

Glu Phe Glu Glu Ser Tyr Val Gln Ala Val Met Gly Ala Pro Arg Thr
340 345 350

Cys Pro Glu Gly Ser Trp Cys Gly Thr Asn Gln Leu Cys Arg Glu Cys
355 360 365

His Ala Phe Thr Thr Trp Asn Met Pro Glu Leu Gly Ala Phe Ser Met
370 375 380

Ser Ala Ala Tyr Asn Val Tyr Glu Ala Val Tyr Ala Val Ala His Gly
385 390 395 400

Leu His Gln Leu Leu Gly Cys Thr Ser Gly Thr Cys Ala Arg Gly Pro
405 410 415

Val Tyr Pro Trp Gln Leu Leu Gln Gln Ile Tyr Lys Val Asn Phe Leu
420 425 430

MON-0301.ST25.txt

Leu His Lys Lys Thr Val Ala Phe Asp Asp Lys Gly Asp Pro Leu Gly
 435 440 445

Tyr Tyr Asp Ile Ile Ala Trp Asp Trp Asn Gly Pro Glu Trp Thr Phe
 450 455 460

Glu Val Ile Gly Ser Ala Ser Leu Ser Pro Val His Leu Asp Ile Asn
 465 470 475 480

Lys Thr Lys Ile Gln Trp His Gly Lys Asn Asn Gln Val Pro Val Ser
 485 490 495

Val Cys Thr Arg Asp Cys Leu Glu Gly His His Arg Leu Val Met Gly
 500 505 510

Ser His His Cys Cys Phe Glu Cys Met Pro Cys Glu Ala Gly Thr Phe
 515 520 525

Leu Asn Thr Ser Glu Leu His Thr Cys Gln Pro Cys Gly Thr Glu Glu
 530 535 540

Trp Ala Pro Glu Gly Ser Ser Ala Cys Phe Ser Arg Thr Val Glu Phe
 545 550 555 560

Leu Gly Trp His Glu Pro Ile Ser Leu Val Leu Leu Ala Ala Asn Thr
 565 570 575

Leu Leu Leu Leu Leu Ile Gly Thr Ala Gly Leu Phe Ala Trp Arg
 580 585 590

Leu His Thr Pro Val Val Arg Ser Ala Gly Gly Arg Leu Cys Phe Leu
 595 600 605

Met Leu Gly Ser Leu Val Ala Gly Ser Cys Ser Leu Tyr Ser Phe Phe
 610 615 620

Gly Lys Pro Thr Val Pro Ala Cys Leu Leu Arg Gln Pro Leu Phe Ser
 625 630 635 640

Leu Gly Phe Ala Ile Phe Leu Ser Cys Leu Thr Ile Arg Ser Phe Gln
 645 650 655

Leu Val Ile Ile Phe Lys Phe Ser Thr Lys Val Pro Thr Phe Tyr His
 660 665 670

Thr Trp Ala Gln Asn His Gly Ala Gly Ile Phe Val Ile Val Ser Ser
 675 680 685

Thr Val His Leu Phe Leu Cys Leu Thr Trp Leu Ala Met Trp Thr Pro
 690 695 700

Arg Pro Thr Arg Glu Tyr Gln Arg Phe Pro His Leu Val Ile Leu Glu
 705 710 715 720

Cys Thr Glu Val Asn Ser Val Gly Phe Leu Val Ala Phe Ala His Asn
725 730 735

Ile Leu Leu Ser Ile Ser Thr Phe Val Cys Ser Tyr Leu Gly Lys Glu
740 745 750

Leu Pro Glu Asn Tyr Asn Glu Ala Lys Cys Val Thr Phe Ser Leu Leu
755 760 } 765

Leu His Phe Val Ser Trp Ile Ala Phe Phe Thr Met Ser Ser Ile Tyr
770 775 780

Gln Gly Ser Tyr Leu Pro Ala Val Asn Val Leu Ala Gly Leu Ala Thr
785 790 795 800

Leu Ser Gly Gly Phe Ser Gly Tyr Phe Leu Pro Lys Cys Tyr Val Ile
805 810 815

Leu Cys Arg Pro Glu Leu Asn Asn Thr Glu His Phe Gln Ala Ser Ile
820 825 830

Gln Asp Tyr Thr Arg Arg Cys Gly Thr Thr
835 840

<210> 16
<211> 840
<212> PRT
<213> Rattus rattus

<400> 16

Met Leu Phe Trp Ala Ala His Leu Leu Leu Ser Leu Gln Leu Val Tyr
1 5 10 15

Cys Trp Ala Phe Ser Cys Gln Arg Thr Glu Ser Ser Pro Gly Phe Ser
20 25 30

Leu Pro Gly Asp Phe Leu Leu Ala Gly Leu Phe Ser Leu His Gly Asp
35 40 45

Cys Leu Gln Val Arg His Arg Pro Leu Val Thr Ser Cys Asp Arg Pro
50 55 60

Asp Ser Phe Asn Gly His Gly Tyr His Leu Phe Gln Ala Met Arg Phe
65 70 75 80

Thr Val Glu Glu Ile Asn Asn Ser Ser Ala Leu Leu Pro Asn Ile Thr
85 90 95

Leu Gly Tyr Glu Leu Tyr Asp Val Cys Ser Glu Ser Ala Asn Val Tyr
100 105 110

Ala Thr Leu Arg Val Leu Ala Leu Gln Gly Pro Arg His Ile Glu Ile

MON-0301.ST25.txt

115

120

125

Gln Lys Asp Leu Arg Asn His Ser Ser Lys Val Val Ala Phe Ile Gly
130 135 140

Pro Asp Asn Thr Asp His Ala Val Thr Thr Ala Ala Leu Leu Gly Pro
145 150 155 160

Phe Leu Met Pro Leu Val Ser Tyr Glu Ala Ser Ser Val Val Leu Ser
165 170 175

Ala Lys Arg Lys Phe Pro Ser Phe Leu Arg Thr Val Pro Ser Asp Arg
180 185 190

His Gln Val Glu Val Met Val Gln Leu Leu Gln Ser Phe Gly Trp Val
195 200 205

Trp Ile Ser Leu Ile Gly Ser Tyr Gly Asp Tyr Gly Gln Leu Gly Val
210 215 220

Gln Ala Leu Glu Glu Leu Ala Val Pro Arg Gly Ile Cys Val Ala Phe
225 230 235 240

Lys Asp Ile Val Pro Phe Ser Ala Arg Val Gly Asp Pro Arg Met Gln
245 250 255

Ser Met Met Gln His Leu Ala Gln Ala Arg Thr Thr Val Val Val Val
260 265 270

Phe Ser Asn Arg His Leu Ala Arg Val Phe Phe Arg Ser Val Val Leu
275 280 285

Ala Asn Leu Thr Gly Lys Val Trp Val Ala Ser Glu Asp Trp Ala Ile
290 295 300

Ser Thr Tyr Ile Thr Ser Val Thr Gly Ile Gln Gly Ile Gly Thr Val
305 310 315 320

Leu Gly Val Ala Val Gln Gln Arg Gln Val Pro Gly Leu Lys Glu Phe
325 330 335

Glu Glu Ser Tyr Val Arg Ala Val Thr Ala Ala Pro Ser Ala Cys Pro
340 345 350

Glu Gly Ser Trp Cys Ser Thr Asn Gln Leu Cys Arg Glu Cys His Thr
355 360 365

Phe Thr Thr Arg Asn Met Pro Thr Leu Gly Ala Phe Ser Met Ser Ala
370 375 380

Ala Tyr Arg Val Tyr Glu Ala Val Tyr Ala Val Ala His Gly Leu His
385 390 395 400

MON-0301.ST25.txt

Gln Leu Leu Gly Cys Thr Ser Glu Ile Cys Ser Arg Gly Pro Val Tyr
405 410 415

Pro Trp Gln Leu Leu Gln Gln Ile Tyr Lys Val Asn Phe Leu Leu His
420 425 430

Glu Asn Thr Val Ala Phe Asp Asp Asn Gly Asp Thr Leu Gly Tyr Tyr
435 440 445

Asp Ile Ile Ala Trp Asp Trp Asn Gly Pro Glu Trp Thr Phe Glu Ile
450 455 460

Ile Gly Ser Ala Ser Leu Ser Pro Val His Leu Asp Ile Asn Lys Thr
465 470 475 480

Lys Ile Gln Trp His Gly Lys Asn Asn Gln Val Pro Val Ser Val Cys
485 490 495

Thr Thr Asp Cys Leu Ala Gly His His Arg Val Val Val Gly Ser His
500 505 510

His Cys Cys Phe Glu Cys Val Pro Cys Glu Ala Gly Thr Phe Leu Asn
515 520 525

Met Ser Glu Leu His Ile Cys Gln Pro Cys Gly Thr Glu Glu Trp Ala
530 535 540

Pro Lys Glu Ser Thr Thr Cys Phe Pro Arg Thr Val Glu Phe Leu Ala
545 550 555 560

Trp His Glu Pro Ile Ser Leu Val Leu Ile Ala Ala Asn Thr Leu Leu
565 570 575

Leu Leu Leu Leu Val Gly Thr Ala Gly Leu Phe Ala Trp His Phe His.
580 585 590

Thr Pro Val Val Arg Ser Ala Gly Gly Arg Leu Cys Phe Leu Met Leu
595 600 605

Gly Ser Leu Val Ala Gly Ser Cys Ser Phe Tyr Ser Phe Phe Gly Glu
610 615 620

Pro Thr Val Pro Ala Cys Leu Leu Arg Gln Pro Leu Phe Ser Leu Gly
625 630 635 640

Phe Ala Ile Phe Leu Ser Cys Leu Thr Ile Arg Ser Phe Gln Leu Val
645 650 655

Ile Ile Phe Lys Phe Ser Thr Lys Val Pro Thr Phe Tyr Arg Thr Trp
660 665 670

Ala Gln Asn His Gly Ala Gly Leu Phe Val Ile Val Ser Ser Thr Val

MON-0301.ST25.txt

675

680

685

His Leu Leu Ile Cys Leu Thr Trp Leu Val Met Trp Thr Pro Arg Pro
690 695 700

Thr Arg Glu Tyr Gln Arg Phe Pro His Leu Val Ile Leu Glu Cys Thr
705 710 715 720

Glu Val Asn Ser Val Gly Phe Leu Leu Ala Phe Thr His Asn Ile Leu
725 730 735

Leu Ser Ile Ser Thr Phe Val Cys Ser Tyr Leu Gly Lys Glu Leu Pro
740 745 750

Glu Asn Tyr Asn Glu Ala Lys Cys Val Thr Phe Ser Leu Leu Leu Asn
755 760 765

Phe Val Ser Trp Ile Ala Phe Phe Thr Met Ala Ser Ile Tyr Gln Gly
770 775 780

Ser Tyr Leu Pro Ala Val Asn Val Leu Ala Gly Leu Thr Thr Leu Ser
785 790 795 800

Gly Gly Phe Ser Gly Tyr Phe Leu Pro Lys Cys Tyr Val Ile Leu Cys
805 810 815

Arg Pro Glu Leu Asn Asn Thr Glu His Phe Gln Ala Ser Ile Gln Asp
820 825 830

Tyr Thr Arg Arg Cys Gly Thr Thr
835 840

<210> 17

<211> 841

<212> PRT

<213> Homo sapiens

<400> 17

Met Leu Leu Cys Thr Ala Arg Leu Val Gly Leu Gln Leu Leu Ile Ser
1 5 10 15

Cys Cys Trp Ala Phe Ala Cys His Ser Thr Glu Ser Ser Pro Asp Phe
20 25 30

Thr Leu Pro Gly Asp Tyr Leu Leu Ala Gly Leu Phe Pro Leu His Ser
35 40 45

Gly Cys Leu Gln Val Arg His Arg Pro Glu Val Thr Leu Cys Asp Arg
50 55 60

Ser Cys Ser Phe Asn Glu His Gly Tyr His Leu Phe Gln Ala Met Arg
65 70 75 80

MON-0301.ST25.txt

Leu Gly Val Glu Glu Ile Asn Asn Ser Thr Ala Leu Leu Pro Asn Ile
85 90 95

Thr Leu Gly Tyr Gln Leu Tyr Asp Val Cys Ser Asp Ser Ala Asn Val
100 105 110

Tyr Ala Thr Leu Arg Val Leu Ser Leu Pro Gly Gln His His Ile Glu
115 120 125

Leu Gln Gly Asp Leu Leu His Tyr Ser Pro Thr Val Leu Ala Val Ile
130 135 140

Gly Pro Asp Ser Thr Asn Arg Ala Ala Thr Thr Ala Ala Leu Leu Ser
145 150 155 160

Pro Phe Leu Val Pro Met Ile Ser Tyr Ala Ala Ser Ser Glu Thr Leu
165 170 175

Ser Val Lys Arg Gln Tyr Pro Ser Phe Leu Arg Thr Ile Pro Asn Asp
180 185 190

Lys Tyr Gln Val Glu Thr Met Val Leu Leu Leu Gln Lys Phe Gly Trp
195 200 205

Thr Trp Ile Ser Leu Val Gly Ser Ser Asp Asp Tyr Gly Gln Leu Gly
210 215 220

Val Gln Ala Leu Glu Asn Gln Ala Thr Gly Gln Gly Ile Cys Ile Ala
225 230 235 240

Phe Lys Asp Ile Met Pro Phe Ser Ala Gln Val Gly Asp Glu Arg Met
245 250 255

Gln Cys Leu Met Arg His Leu Ala Gln Ala Gly Ala Thr Val Val Val
260 265 270

Val Phe Ser Ser Arg Gln Leu Ala Arg Val Phe Phe Glu Ser Val Val
275 280 285

Leu Thr Asn Leu Thr Gly Lys Val Trp Val Ala Ser Glu Ala Trp Ala
290 295 300

Leu Ser Arg His Ile Thr Gly Val Pro Gly Ile Gln Arg Ile Gly Met
305 310 315 320

Val Leu Gly Val Ala Ile Gln Lys Arg Ala Val Pro Gly Leu Lys Ala
325 330 335

Phe Glu Glu Ala Tyr Ala Arg Ala Asp Lys Lys Ala Pro Arg Pro Cys
340 345 350

His Lys Gly Ser Trp Cys Ser Ser Asn Gln Leu Cys Arg Glu Cys Gln
355 360 365

MON-0301.ST25.txt

Ala Phe Met Ala His Thr Met Pro Lys Leu Lys Ala Phe Ser Met Ser
370 375 380

Ser Ala Tyr Asn Ala Tyr Arg Ala Val Tyr Ala Val Ala His Gly Leu
385 390 395 400

His Gln Leu Leu Gly Cys Ala Ser Gly Ala Cys Ser Arg Gly Arg Val
405 410 415

Tyr Pro Trp Gln Leu Leu Glu Gln Ile His Lys Val His Phe Leu Leu
420 425 430

His Lys Asp Thr Val Ala Phe Asn Asp Asn Arg Asp Pro Leu Ser Ser
435 440 445

Tyr Asn Ile Ile Ala Trp Asp Trp Asn Gly Pro Lys Trp Thr Phe Thr
450 455 460

Val Leu Gly Ser Ser Thr Trp Ser Pro Val Gln Leu Asn Ile Asn Glu
465 470 475 480

Thr Lys Ile Gln Trp His Gly Lys Asp Asn Gln Val Pro Lys Ser Val
485 490 495

Cys Ser Ser Asp Cys Leu Glu Gly His Gln Arg Val Val Thr Gly Phe
500 505 510

His His Cys Cys Phe Glu Cys Val Pro Cys Gly Ala Gly Thr Phe Leu
515 520 525

Asn Lys Ser Asp Leu Tyr Arg Cys Gln Pro Cys Gly Lys Glu Glu Trp
530 535 540

Ala Pro Glu Gly Ser Gln Thr Cys Phe Pro Arg Thr Val Val Phe Leu
545 550 555 560

Ala Leu Arg Glu His Thr Ser Trp Val Leu Leu Ala Ala Asn Thr Leu
565 570 575

Leu Leu Leu Leu Leu Gly Thr Ala Gly Leu Phe Ala Trp His Leu
580 585 590

Asp Thr Pro Val Val Arg Ser Ala Gly Gly Arg Leu Cys Phe Leu Met
595 600 605

Leu Gly Ser Leu Ala Ala Gly Ser Gly Ser Leu Tyr Gly Phe Phe Gly
610 615 620

Glu Pro Thr Arg Pro Ala Cys Leu Leu Arg Gln Ala Leu Phe Ala Leu
625 630 635 640

MON-0301.ST25.txt

Gly Phe Thr Ile Phe Leu Ser Cys Leu Thr Val Arg Ser Phe Gln Leu
645 650 655

Ile Ile Ile Phe Lys Phe Ser Thr Lys Val Pro Thr Phe Tyr His Ala
660 665 670

Trp Val Gln Asn His Gly Ala Gly Leu Phe Val Met Ile Ser Ser Ala
675 680 685

Ala Gln Leu Leu Ile Cys Leu Thr Trp Leu Val Val Trp Thr Pro Leu
690 695 700

Pro Ala Arg Glu Tyr Gln Arg Phe Pro His Leu Val Met Leu Glu Cys
705 710 715 720

Thr Glu Thr Asn Ser Leu Gly Phe Ile Leu Ala Phe Leu Tyr Asn Gly
725 730 735

Leu Leu Ser Ile Ser Ala Phe Ala Cys Ser Tyr Leu Gly Lys Asp Leu
740 745 750

Pro Glu Asn Tyr Asn Glu Ala Lys Cys Val Thr Phe Ser Leu Leu Phe
755 760 765

Asn Phe Val Ser Trp Ile Ala Phe Phe Thr Thr Ala Ser Val Tyr Asp
770 775 780

Gly Lys Tyr Leu Pro Ala Ala Asn Met Met Ala Gly Leu Ser Ser Leu
785 790 795 800

Ser Ser Gly Phe Gly Gly Tyr Phe Leu Pro Lys Cys Tyr Val Ile Leu
805 810 815

Cys Arg Pro Asp Leu Asn Ser Thr Glu His Phe Gln Ala Ser Ile Gln
820 825 830

Asp Tyr Thr Arg Arg Cys Gly Ser Thr
835 840

<210> 18

<211> 843

<212> PRT

<213> Mus musculus

<400> 18

Met Gly Pro Gln Ala Arg Thr Leu His Leu Leu Phe Leu Leu His
1 5 10 15

Ala Leu Pro Lys Pro Val Met Leu Val Gly Asn Ser Asp Phe His Leu
20 25 30

Ala Gly Asp Tyr Leu Leu Gly Leu Phe Thr Leu His Ala Asn Val
35 40 45

"MON-0301.ST25.txt

Lys Ser Val Ser His Leu Ser Tyr Leu Gln Val Pro Lys Cys Asn Glu
50 55 60

Tyr Asn Met Lys Val Leu Gly Tyr Asn Leu Met Gln Ala Met Arg Phe
65 70 75 80

Ala Val Glu Glu Ile Asn Asn Cys Ser Ser Leu Leu Pro Gly Val Leu
85 90 95

Leu Gly Tyr Glu Met Val Asp Val Cys Tyr Leu Ser Asn Asn Ile Gln
100 105 110

Pro Gly Leu Tyr Phe Leu Ser Gln Ile Asp Asp Phe Leu Pro Ile Leu
115 120 125

Lys Asp Tyr Ser Gln Tyr Arg Pro Gln Val Val Ala Val Ile Gly Pro
130 135 140

Asp Asn Ser Glu Ser Ala Ile Thr Val Ser Asn Ile Leu Ser Tyr Phe
145 150 155 160

Leu Val Pro Gln Val Thr Tyr Ser Ala Ile Thr Asp Lys Leu Arg Asp
165 170 175

Lys Arg Arg Phe Pro Ala Met Leu Arg Thr Val Pro Ser Ala Thr His
180 185 190

His Ile Glu Ala Met Val Gln Leu Met Val His Phe Gln Trp Asn Trp
195 200 205

Ile Val Val Leu Val Ser Asp Asp Asp Tyr Gly Arg Glu Asn Ser His
210 215 220

Leu Leu Ser Gln Arg Leu Thr Asn Thr Gly Asp Ile Cys Ile Ala Phe
225 230 235 240

Gln Glu Val Leu Pro Val Pro Glu Pro Asn Gln Ala Val Arg Pro Glu
245 250 255

Glu Gln Asp Gln Leu Asp Asn Ile Leu Asp Lys Leu Arg Arg Thr Ser
260 265 270

Ala Arg Val Val Val Ile Phe Ser Pro Glu Leu Ser Leu His Asn Phe
275 280 285

Phe Arg Glu Val Leu Arg Trp Asn Phe Thr Gly Phe Val Trp Ile Ala
290 295 300

Ser Glu Ser Trp Ala Ile Asp Pro Val Leu His Asn Leu Thr Glu Leu
305 310 315 320

Arg His Thr Gly Thr Phe Leu Gly Val Thr Ile Gln Arg Val Ser Ile

"MON-0301.ST25.txt

325

330

335

Pro Gly Phe Ser Gln Phe Arg Val Arg His Asp Lys Pro Glu Tyr Pro
 340 345 350

Met Pro Asn Glu Thr Ser Leu Arg Thr Thr Cys Asn Gln Asp Cys Asp
 355 360 365

Ala Cys Met Asn Ile Thr Glu Ser Phe Asn Asn Val Leu Met Leu Ser
 370 375 380

Gly Glu Arg Val Val Tyr Ser Val Tyr Ser Ala Val Tyr Ala Val Ala
 385 390 395 400

His Thr Leu His Arg Leu Leu His Cys Asn Gln Val Arg Cys Thr Lys
 405 410 415

Gln Ile Val Tyr Pro Trp Gln Leu Leu Arg Glu Ile Trp His Val Asn
 420 425 430

Phe Thr Leu Leu Gly Asn Gln Leu Phe Phe Asp Glu Gln Gly Asp Met
 435 440 445

Pro Met Leu Leu Asp Ile Ile Gln Trp Gln Trp Gly Leu Ser Gln Asn
 450 455 460

Pro Phe Gln Ser Ile Ala Ser Tyr Ser Pro Thr Glu Thr Arg Leu Thr
 465 470 475 480

Tyr Ile Ser Asn Val Ser Trp Tyr Thr Pro Asn Asn Thr Val Pro Ile
 485 490 495

Ser Met Cys Ser Lys Ser Cys Gln Pro Gly Gln Met Lys Lys Pro Ile
 500 505 510

Gly Leu His Pro Cys Cys Phe Glu Cys Val Asp Cys Pro Pro Gly Thr
 515 520 525

Tyr Leu Asn Arg Ser Val Asp Glu Phe Asn Cys Leu Ser Cys Pro Gly
 530 535 540

Ser Met Trp Ser Tyr Lys Asn Asn Ile Ala Cys Phe Lys Arg Arg Leu
 545 550 555 560

Ala Phe Leu Glu Trp His Glu Val Pro Thr Ile Val Val Thr Ile Leu
 565 570 575

Ala Ala Leu Gly Phe Ile Ser Thr Leu Ala Ile Leu Leu Ile Phe Trp
 580 585 590

Arg His Phe Gln Thr Pro Met Val Arg Ser Ala Gly Gly Pro Met Cys
 595 600 605

MON-0301.ST25.txt

Phe Leu Met Leu Val Pro Leu Leu Leu Ala Phe Gly Met Val Pro Val
610 615 620

Tyr Val Gly Pro Pro Thr Val Phe Ser Cys Phe Cys Arg Gln Ala Phe
625 630 635 640

Phe Thr Val Cys Phe Ser Val Cys Leu Ser Cys Ile Thr Val Arg Ser
645 650 655

Phe Gln Ile Val Cys Val Phe Lys Met Ala Arg Arg Leu Pro Ser Ala
660 665 670

Tyr Gly Phe Trp Met Arg Tyr His Gly Pro Tyr Val Phe Val Ala Phe
675 680 685

Ile Thr Ala Val Lys Val Ala Leu Val Ala Gly Asn Met Leu Ala Thr
690 695 700

Thr Ile Asn Pro Ile Gly Arg Thr Asp Pro Asp Asp Pro Asn Ile Ile
705 710 715 720

Ile Leu Ser Cys His Pro Asn Tyr Arg Asn Gly Leu Leu Phe Asn Thr
725 730 735

Ser Met Asp Leu Leu Leu Ser Val Leu Gly Phe Ser Phe Ala Tyr Val
740 745 750

Gly Lys Glu Leu Pro Thr Asn Tyr Asn Glu Ala Lys Phe Ile Thr Leu
755 760 765

Ser Met Thr Phe Ser Phe Thr Ser Ser Ile Ser Leu Cys Thr Phe Met
770 775 780

Ser Val His Asp Gly Val Leu Val Thr Ile Met Asp Leu Leu Val Thr
785 790 795 800

Val Leu Asn Phe Leu Ala Ile Gly Leu Gly Tyr Phe Gly Pro Lys Cys
805 810 815

Tyr Met Ile Leu Phe Tyr Pro Glu Arg Asn Thr Ser Ala Tyr Phe Asn
820 825 830

Ser Met Ile Gln Gly Tyr Thr Met Arg Lys Ser
835 840

<210> 19
<211> 843
<212> PRT
<213> Rattus rattus

<400> 19

Met Gly Pro Gln Ala Arg Thr Leu Cys Leu Leu Ser Leu Leu His
1 5 10 15

Val Leu Pro Lys Pro Gly Lys Leu Val Glu Asn Ser Asp Phe His Leu
20 25 30

Ala Gly Asp Tyr Leu Leu Gly Gly Leu Phe Thr Leu His Ala Asn Val
35 40 45

Lys Ser Ile Ser His Leu Ser Tyr Leu Gln Val Pro Lys Cys Asn Glu
50 55 60

Phe Thr Met Lys Val Leu Gly Tyr Asn Leu Met Gln Ala Met Arg Phe
65 70 75 80

Ala Val Glu Glu Ile Asn Asn Cys Ser Ser Leu Leu Pro Gly Val Leu
85 90 95

Leu Gly Tyr Glu Met Val Asp Val Cys Tyr Leu Ser Asn Asn Ile His
100 105 110

Pro Gly Leu Tyr Phe Leu Ala Gln Asp Asp Asp Leu Leu Pro Ile Leu
115 120 125

Lys Asp Tyr Ser Gln Tyr Met Pro His Val Val Ala Val Ile Gly Pro
130 135 140

Asp Asn Ser Glu Ser Ala Ile Thr Val Ser Asn Ile Leu Ser His Phe
145 150 155 160

Leu Ile Pro Gln Ile Thr Tyr Ser Ala Ile Ser Asp Lys Leu Arg Asp
165 170 175

Lys Arg His Phe Pro Ser Met Leu Arg Thr Val Pro Ser Ala Thr His
180 185 190

His Ile Glu Ala Met Val Gln Leu Met Val His Phe Gln Trp Asn Trp
195 200 205

Ile Val Val Leu Val Ser Asp Asp Asp Tyr Gly Arg Glu Asn Ser His
210 215 220

Leu Leu Ser Gln Arg Leu Thr Lys Thr Ser Asp Ile Cys Ile Ala Phe
225 230 235 240

Gln Glu Val Leu Pro Ile Pro Glu Ser Ser Gln Val Met Arg Ser Glu
245 250 255

Glu Gln Arg Gln Leu Asp Asn Ile Leu Asp Lys Leu Arg Arg Thr Ser
260 265 270

Ala Arg Val Val Val Phe Ser Pro Glu Leu Ser Leu Tyr Ser Phe
275 280 285

MON-0301.ST25.txt

Phe His Glu Val Leu Arg Trp Asn Phe Thr Gly Phe Val Trp Ile Ala

290 295

300

Ser Glu Ser Trp Ala Ile Asp Pro Val Leu His Asn Leu Thr Glu Leu

305

310

315

320

Arg His Thr Gly Thr Phe Leu Gly Val Thr Ile Gln Arg Val Ser Ile

325

330

335

Pro Gly Phe Ser Gln Phe Arg Val Arg Arg Asp Lys Pro Gly Tyr Pro

340

345

350

Val Pro Asn Thr Thr Asn Leu Arg Thr Thr Cys Asn Gln Asp Cys Asp

355

360

365

Ala Cys Leu Asn Thr Thr Lys Ser Phe Asn Asn Ile Leu Ile Leu Ser

370

375

380

Gly Glu Arg Val Val Tyr Ser Val Tyr Ser Ala Val Tyr Ala Val Ala

385

390

395

400

His Ala Leu His Arg Leu Leu Gly Cys Asn Arg Val Arg Cys Thr Lys

405

410

415

Gln Lys Val Tyr Pro Trp Gln Leu Leu Arg Glu Ile Trp His Val Asn

420

425

430

Phe Thr Leu Leu Gly Asn Arg Leu Phe Phe Asp Gln Gln Gly Asp Met

435

440

445

Pro Met Leu Leu Asp Ile Ile Gln Trp Gln Trp Asp Leu Ser Gln Asn

450

455

460

Pro Phe Gln Ser Ile Ala Ser Tyr Ser Pro Thr Ser Lys Arg Leu Thr

465

470

475

480

Tyr Ile Asn Asn Val Ser Trp Tyr Thr Pro Asn Asn Thr Val Pro Val

485

490

495

Ser Met Cys Ser Lys Ser Cys Gln Pro Gly Gln Met Lys Lys Ser Val

500

505

510

Gly Leu His Pro Cys Cys Phe Glu Cys Leu Asp Cys Met Pro Gly Thr

515

520

525

Tyr Leu Asn Arg Ser Ala Asp Glu Phe Asn Cys Leu Ser Cys Pro Gly

530

535

540

Ser Met Trp Ser Tyr Lys Asn Asp Ile Thr Cys Phe Gln Arg Arg Pro

545

550

555

560

Thr Phe Leu Glu Trp His Glu Val Pro Thr Ile Val Val Ala Ile Leu

565

570

575

Ala Ala Leu Gly Phe Phe Ser Thr Leu Ala Ile Leu Phe Ile Phe Trp
580 585 590

Arg His Phe Gln Thr Pro Met Val Arg Ser Ala Gly Gly Pro Met Cys
595 600 605

Phe Leu Met Leu Val Pro Leu Leu Leu Ala Phe Gly Met Val Pro Val
610 615 620

Tyr Val Gly Pro Pro Thr Val Phe Ser Cys Phe Cys Arg Gln Ala Phe
625 630 635 640

Phe Thr Val Cys Phe Ser Ile Cys Leu Ser Cys Ile Thr Val Arg Ser
645 650 655

Phe Gln Ile Val Cys Val Phe Lys Met Ala Arg Arg Leu Pro Ser Ala
660 665 670

Tyr Ser Phe Trp Met Arg Tyr His Gly Pro Tyr Val Phe Val Ala Phe
675 680 685

Ile Thr Ala Ile Lys Val Ala Leu Val Val Gly Asn Met Leu Ala Thr
690 695 700

Thr Ile Asn Pro Ile Gly Arg Thr Asp Pro Asp Asp Pro Asn Ile Met
705 710 715 720

Ile Leu Ser Cys His Pro Asn Tyr Arg Asn Gly Leu Leu Phe Asn Thr
725 730 735

Ser Met Asp Leu Leu Leu Ser Val Leu Gly Phe Ser Phe Ala Tyr Met
740 745 750

Gly Lys Glu Leu Pro Thr Asn Tyr Asn Glu Ala Lys Phe Ile Thr Leu
755 760 765

Ser Met Thr Phe Ser Phe Thr Ser Ser Ile Ser Leu Cys Thr Phe Met
770 775 780

Ser Val His Asp Gly Val Leu Val Thr Ile Met Asp Leu Leu Val Thr
785 790 795 800

Val Leu Asn Phe Leu Ala Ile Gly Leu Gly Tyr Phe Gly Pro Lys Cys
805 810 815

Tyr Met Ile Leu Phe Tyr Pro Glu Arg Asn Thr Ser Ala Tyr Phe Asn
820 825 830

Ser Met Ile Gln Gly Tyr Thr Met Arg Lys Ser
835 840

MON-0301.ST25.txt

<210> 20
<211> 839
<212> PRT
<213> Homo sapiens

<400> 20

Met Gly Pro Arg Ala Lys Thr Ile Cys Ser Leu Phe Phe Leu Leu Trp
1 5 10 15

Val Leu Ala Glu Pro Ala Glu Asn Ser Asp Phe Tyr Leu Pro Gly Asp
20 25 30

Tyr Leu Leu Gly Gly Leu Phe Ser Leu His Ala Asn Met Lys Gly Ile
35 40 45

Val His Leu Asn Phe Leu Gln Val Pro Met Cys Lys Glu Tyr Glu Val
50 55 60

Lys Val Ile Gly Tyr Asn Leu Met Gln Ala Met Arg Phe Ala Val Glu
65 70 75 80

Glu Ile Asn Asn Asp Ser Ser Leu Leu Pro Gly Val Leu Leu Gly Tyr
85 90 95

Glu Ile Val Asp Val Cys Tyr Ile Ser Asn Asn Val Gln Pro Val Leu
100 105 110

Tyr Phe Leu Ala His Glu Asp Asn Leu Leu Pro Ile Gln Glu Asp Tyr
115 120 125

Ser Asn Tyr Ile Ser Arg Val Val Ala Val Ile Gly Pro Asp Asn Ser
130 135 140

Glu Ser Val Met Thr Val Ala Asn Phe Leu Ser Leu Phe Leu Leu Pro
145 150 155 160

Gln Ile Thr Tyr Ser Ala Ile Ser Asp Glu Leu Arg Asp Lys Val Arg
165 170 175

Phe Pro Ala Leu Leu Arg Thr Thr Pro Ser Ala Asp His His Val Glu
180 185 190

Ala Met Val Gln Leu Met Leu His Phe Arg Trp Asn Trp Ile Ile Val
195 200 205

Leu Val Ser Ser Asp Thr Tyr Gly Arg Asp Asn Gly Gln Leu Leu Gly
210 215 220

Glu Arg Val Ala Arg Arg Asp Ile Cys Ile Ala Phe Gln Glu Thr Leu
225 230 235 240

Pro Thr Leu Gln Pro Asn Gln Asn Met Thr Ser Glu Glu Arg Gln Arg
245 250 255

MON-0301.ST25.txt

Leu Val Thr Ile Val Asp Lys Leu Gln Gln Ser Thr Ala Arg Val Val
260 265 270

Val Val Phe Ser Pro Asp Leu Thr Leu Tyr His Phe Phe Asn Glu Val
275 280 285

Leu Arg Gln Asn Phe Thr Gly Ala Val Trp Ile Ala Ser Glu Ser Trp
290 295 300

Ala Ile Asp Pro Val Leu His Asn Leu Thr Glu Leu Gly His Leu Gly
305 310 315 320

Thr Phe Leu Gly Ile Thr Ile Gln Ser Val Pro Ile Pro Gly Phe Ser
325 330 335

Glu Phe Arg Glu Trp Gly Pro Gln Ala Gly Pro Pro Pro Leu Ser Arg
340 345 350

Thr Ser Gln Ser Tyr Thr Cys Asn Gln Glu Cys Asp Asn Cys Leu Asn
355 360 365

Ala Thr Leu Ser Phe Asn Thr Ile Leu Arg Leu Ser Gly Glu Arg Val
370 375 380

Val Tyr Ser Val Tyr Ser Ala Val Tyr Ala Val Ala His Ala Leu His
385 390 395 400

Ser Leu Leu Gly Cys Asp Lys Ser Thr Cys Thr Lys Arg Val Val Tyr
405 410 415

Pro Trp Gln Leu Leu Glu Glu Ile Trp Lys Val Asn Phe Thr Leu Leu
420 425 430

Asp His Gln Ile Phe Phe Asp Pro Gln Gly Asp Val Ala Leu His Leu
435 440 445

Glu Ile Val Gln Trp Gln Trp Asp Arg Ser Gln Asn Pro Phe Gln Ser
450 455 460

Val Ala Ser Tyr Tyr Pro Leu Gln Arg Gln Leu Lys Asn Ile Gln Asp
465 470 475 480

Ile Ser Trp His Thr Val Asn Asn Thr Ile Pro Met Ser Met Cys Ser
485 490 495

Lys Arg Cys Gln Ser Gly Gln Lys Lys Lys Pro Val Gly Ile His Val
500 505 510

Cys Cys Phe Glu Cys Ile Asp Cys Leu Pro Gly Thr Phe Leu Asn His
515 520 525

Thr Glu Asp Glu Tyr Glu Cys Gln Ala Cys Pro Asn Asn Glu Trp Ser

530

535

MON-0301.ST25.txt

540

Tyr Gln Ser Glu Thr Ser Cys Phe Lys Arg Gln Leu Val Phe Leu Glu
545 550 555 560

Trp His Glu Ala Pro Thr Ile Ala Val Ala Leu Leu Ala Ala Leu Gly
565 570 575

Phe Leu Ser Thr Leu Ala Ile Leu Val Ile Phe Trp Arg His Phe Gln
580 585 590

Thr Pro Ile Val Arg Ser Ala Gly Gly Pro Met Cys Phe Leu Met Leu
595 600 605

Thr Leu Leu Leu Val Ala Tyr Met Val Val Pro Val Tyr Val Gly Pro
610 615 620

Pro Lys Val Ser Thr Cys Leu Cys Arg Gln Ala Leu Phe Pro Leu Cys
625 630 635 640

Phe Thr Ile Cys Ile Ser Cys Ile Ala Val Arg Ser Phe Gln Ile Val
645 650 655

Cys Ala Phe Lys Met Ala Ser Arg Phe Pro Arg Ala Tyr Ser Tyr Trp
660 665 670

Val Arg Tyr Gln Gly Pro Tyr Val Ser Met Ala Phe Ile Thr Val Leu
675 680 685

Lys Met Val Ile Val Val Ile Gly Met Leu Ala Thr Gly Leu Ser Pro
690 695 700

Thr Thr Arg Thr Asp Pro Asp Asp Pro Lys Ile Thr Ile Val Ser Cys
705 710 715 720

Asn Pro Asn Tyr Arg Asn Ser Leu Leu Phe Asn Thr Ser Leu Asp Leu
725 730 735

Leu Leu Ser Val Val Gly Phe Ser Phe Ala Tyr Met Gly Lys Glu Leu
740 745 750

Pro Thr Asn Tyr Asn Glu Ala Lys Phe Ile Thr Leu Ser Met Thr Phe
755 760 765

Tyr Phe Thr Ser Ser Val Ser Leu Cys Thr Phe Met Ser Ala Tyr Ser
770 775 780

Gly Val Leu Val Thr Ile Val Asp Leu Leu Val Thr Val Leu Asn Leu
785 790 795 800

Leu Ala Ile Ser Leu Gly Tyr Phe Gly Pro Lys Cys Tyr Met Ile Leu
805 810 815

Phe Tyr Pro Glu Arg Asn Thr Pro Ala Tyr Phe Asn Ser Met Ile Gln
820 825 830

Gly Tyr Thr Met Arg Arg Asp
835

<210> 21
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Overgo probes

<400> 21
actttgagaa catgagtaat gacg 24

<210> 22
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Overgo probes

<400> 22
agtaccggga ctgcgtcgta atta 24

<210> 23
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Overgo probes

<400> 23
cactagggtc atccttgctt tcag 24

<210> 24
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Overgo probes

<400> 24
agtcaagggtg atgggcctga aagc 24

<210> 25
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Overgo probes

<400> 25
atgtgggtgaa ctggctgtac catc 24

<210> 26

MON-0301.ST25.txt

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Overgo probes

<400> 26
ttgaagccct ccacgtgatg gtac 24

<210> 27
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Overgo probes

<400> 27
cacacggta acaagatcac cttc 24

<210> 28
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Overgo probes

<400> 28
agttagcactg ctcggagaag gtga 24

<210> 29
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Overgo probes

<400> 29
atctaccaca tggacgagga ggag 24

<210> 30
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Overgo probes

<400> 30
tgaccaggta cggcgcttcc tcct 24

<210> 31
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Overgo probes

<400> 31
agcgcgtaac gctggccgac ttca 24

MON-0301.ST25.txt

<210> 32
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Overgo probes

<400> 32
ttgctgagca cgttcttgaa gtcg

24

<210> 33
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Overgo probes

<400> 33
cacgcctaca aattcttctt taag

24

<210> 34
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Overgo probes

<400> 34
agtccctggtc catggactta aaga

24

<210> 35
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Overgo probes

<400> 35
cttccactcc tgctgctacg actg

24

<210> 36
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Overgo probes

<400> 36
tgcctcgcag tccacgcagt cgta

24

<210> 37
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Overgo probes

<400> 37

aggtgcgccg cgtcaagggc ttcc

<210> 38
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Overgo probes

<400> 38
tcgttagcagc aggagtgaa gccc

24

<210> 39
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Overgo probes

<400> 39
gttcctggca tggggggagc cggc

24

<210> 40
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Overgo probes

<400> 40
gagcagcaca agcacagccg gctc

24

<210> 41
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Overgo probes

<400> 41
acagcccaact agttcaggcc gcag

24

<210> 42
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Overgo probes

<400> 42
caggccccggg gtccccctgc ggcc

24

<210> 43
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Overgo probes

<400> 43
cccaactgggtt caggcctcg gg

24

<210> 44
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Overgo probes

<400> 44
aaagcaggcc aggggcccccc ccga

24

<210> 45
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Overgo probes

<400> 45
aggcgctggt gcactgccgc acac

24

<210> 46
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Overgo probes

<400> 46
aagctgaccc aggagcgtgt gcgg

24

<210> 47
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Overgo probes

<400> 47
acagaggcac tggtgcaactg ccgc

24

<210> 48
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Overgo probes

<400> 48
tgatccagga gtgcacgcgg cagt

24

<210> 49
<211> 24
<212> DNA
<213> Artificial Sequence

MON-0301.ST25.txt

<220>
<223> Overgo probes

<400> 49
accaatgcca cgctggcctt tctc

24

<210> 50
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Overgo probes

<400> 50
aagtgcaggag gaagcagaga aagg

24

<210> 51
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Overgo probes

<400> 51
tggtacatgc tgccaatgcc acgc

24

<210> 52
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Overgo probes

<400> 52
aagcagagga aagccagcgt ggca

24

<210> 53
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Overgo probes

<400> 53
tacaaccgtg cccgtggcct cacc

24

<210> 54
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Overgo probes

<400> 54
aggccagcat ggcgaaggta aggc

24

<210> 55
<211> 24
<212> DNA

<213> Artificial Sequence MON-0301.ST25.txt

<220>

<223> Overgo probes

<400> 55

tcatcacctg ggtctccttt gtgc

24

<210> 56

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Overgo probes

<400> 56

acattggcca ggaggggcac aaag

24

<210> 57

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Overgo probes

<400> 57

tgcagatggg tgccctcctg ctct

24

<210> 58

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Overgo probes

<400> 58

aggatgccca gcacacagag cagg

24

<210> 59

<211> 9049

<212> DNA

<213> Felis catus

<220>

<221> misc_feature

<222> (14)..(14)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (47)..(47)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (56)..(56)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (67)..(67)

<223> n is a, c, g, or t

MON-0301.ST25.txt

```
<220>
<221> misc_feature
<222> (2113)..(2113)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (2121)..(2121)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (2125)..(2132)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (2138)..(2138)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (4198)..(4198)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (4232)..(4232)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (4237)..(4237)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (4256)..(4256)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (4264)..(4264)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (4272)..(4272)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (4298)..(4298)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (4328)..(4328)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (4341)..(4341)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (4343)..(4343)
<223> n is a, c, g, or t
```

MON-0301.ST25.txt

```

<220>
<221> misc_feature
<222> (4354)..(4354)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (4386)..(4386)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (4389)..(4390)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (4399)..(4456)
<223> n is a, c, g, or t

<400> 59
ctggaaaaaa aggngaaccc aggtgattc accccaaaat ttcatntca gaaaantgag      60
gactggnagg aggtcaactt aaagtcaatt tcattttgtt aactgaggcc caggtaaaaa     120
gttctaaaaac ccacagctcc ctccatatt ctgtccccca gagaagcagt gtccctgcct    180
tcctctgacc cctgcccctc aagacgcctg ggctcccttt ctgagccggg tgaagccgca   240
ggcaccagag cgagaacaga acccacaacc atccagaggg aggggcagcg gccaccacct  300
ggcttgcacc tgtgccttca ccctgcccag ttccctgagta ggaccgcagg cccggaaggc  360
caaggcaaac agcctggttc ctacgactgg gttccagccc cacccctggc acaggcgtga  420
agttggaaag catctggca gcccgtgtct attctattta aacagccgag ctggtcagag  480
ggtgctggct ggcatgcca ggcacaggac ggactggcca gcatgtcact cccggcggct  540
cacctggtcg gctgcagct ctccctctcc tgctgctggg ctctcagctg ccacagcaca  600
gagacgtctg ccgacttcag cctccctggg gattacctcc tcgcaggctt gttccctctg  660
cactctgact gtccggcgt gaggcaccgg cccacggta ccctctgtga caggtgagtg  720
aggggtcccg tgcctcttagg acctctgccc atcctctgtc ctccctcagtg aggatccctg 780
ggttgttgat tgagtggagt tagggccttt tagagagctg agactctaga agctaaacca  840
cgtgttgctt tacctgtctt ccaccctgag gatcacacgt taagtgtctt taccagtcaa  900
aattgaatat gtatcaaaca aaaataaatg gccttccatg ctgaaataac aaaaaacaga  960
cacgcatgga gaacctactt tgtggggcgc ctgggtggcc cagtcggta agtgtctgcc 1020
tcttcgttt ggctcaggtc atgacctcgg ggttcatgag ttcgagcccc gcgtcagctc 1080
cgtgatgagc ctggagcccg ctggaaattc cctccccacc cccacccccc gctcatgcca 1140
gctcgagctc togctcactc tctaaaaata aacttaagag gggcgctgg gtggcgagt 1200
cagttaaagcg tccgacttca gccaggtcac gatcagcaca ttatttcctg gaccttccat 1260
tctcccttcg ctgtacagag cttaacgtaa actccctggc aagacccctt ttctgattt 1320
agaaaggcca gcttattggt ttggttcctg taatagctt aaaaatagaat ccagctgtat 1380
cagggaaacat ttaaaaaatg tatcaaggaa gacctataac agtaaaaata ttttaaaatc 1440

```

| MON-0301.ST25.txt | | | |
|-------------------|--------------|--|------|
| ccagagtgtt | ttcataaaga | cacaggatta cattactcaa ttatTTTaa aggTTTTg | 1500 |
| aaaAGCCGTG | tttcacttgc | catggtaat gattataggc atccgaatga gcctgtggct | 1560 |
| atgacttcag | tctgttcggt | ggaaatgact ctgatgtcat aaactgactc ggcttcgctg | 1620 |
| acaggaaagt | cgtacagaag | aaaagctgtt cgagcccata tgggggtgc gctcaatgtc | 1680 |
| aggaaggggc | gacgtaatgt | gtgcagaaat gggcagctgt cgagagtgaa gaaattggga | 1740 |
| agttggcacg | gaagagggga | ccgagtccga gaaggctgct ggataaagca gagctttgc | 1800 |
| agaagagaag | ggccggctgc | tgtccctatc ctgggtggcg aaccacttag aaacaaggcg | 1860 |
| tcagaattag | agacttcggt | tcatgcaggg agggcggccc aggggggtgg cgtccttgga | 1920 |
| aactctggta | agtttgagat | tgatcccagg ggtcgtggga tggagcctcg catgagactc | 1980 |
| tacactgatc | gatgagaagc | agaagccccct tgtctgtgag gaaggggaca cgagcagttg | 2040 |
| gcacactaaa | acgcaaggac | acgtttctac gagaaaacgg tacatctgtc tgcgacacag | 2100 |
| aaagatcccc | gnnaccagtc | ntcgnnnnnn nnttccgntg ggattccagt cagcagttcc | 2160 |
| cgagaggcac | tgaggaacac | aggccctcac cacgttcaca agtgtcctga tgagagggat | 2220 |
| actaggtaaa | cgaggttcga | caggtgtggt ggttaatttt atacatcaac ctggctaggg | 2280 |
| tacggtgccc | agttgtttgg | ccaaacacca gtctagatgg ggctgtgaag gttaacattt | 2340 |
| aaaccaacag | ggtgagtaaa | gcagatcgct ttccattgtg tgggtgggcc tcataccaatc | 2400 |
| agttgaagac | ctaaaaagaa | aagattgagg tccccccaaa aaggaagaaa ttctgccttc | 2460 |
| gaactcaaca | ctgcagcttt | gaccactgag agcatttcca gcctgcctg caaacgccag | 2520 |
| actcaccagc | cccacaatca | tgtgaaccaa ttccctaaaa taaacttctc ttctctctc | 2580 |
| tctatccaac | tggttctgtt | tctctgcaga accctgactc acgcagcagg ttccctgct | 2640 |
| acaggacttc | atcagccttt | caaccataat atgctcatcc agggaggaat ggTTTGTGGT | 2700 |
| ttctccaagt | tgttaaccgccc | cctccccccc cccccccgccc ccccaaaagg cctgttaaca | 2760 |
| cagctgagtg | tatggtacag | ggcccacagt gaggtcatgg tggtagggg cgggacagat | 2820 |
| gccctcagag | tttcctttct | acccttcccc ccaccccccga cgccaagagg gtctcgca | 2880 |
| ggccttgctc | ctctgagctc | tcagctggc ttctctaca ggcccacag ctcaacgg | 2940 |
| cacggctacc | acctttcca | ggccatgcgg ttggcatcg aggagataaa caactccacg | 3000 |
| gccctcctgc | cgaacgtc | cctggatac cagctgtacg acgtgtgctc ggagtctgcc | 3060 |
| aacgtgtatg | ccacactaaa | cgtgctctcc ctgctggga cacatcacgt agagatccga | 3120 |
| gcagaccctt | cccaactattc | gcctgcccgc ctggctgtca ttgggcctga caccaccaac | 3180 |
| cacgcagcca | ccactgcagc | cctgctgagc cccttcctgg tgccccctgt gagctggagc | 3240 |
| ccgggggcct | gtccatctcc | cctgcccgc ggtccagtgt gggctgaggg ggtgggggg | 3300 |
| tgggcaagag | ctgccatgcc | cactctgagt ctccctgggt gtcacattgc agggggccct | 3360 |
| gcccccttca | cagtccccgc | cccagcatcc ctccctcccc aagtgctgca tccagacctc | 3420 |
| cctgcctcaa | tgtcctgaga | aaaaccgtct ccttgaac tgcgcctt tgctctgccc | 3480 |
| cctccattcc | atctcctctg | tgaagaacgg aacacccttt gtttcccacc tcacacactt | 3540 |

MON-0301.ST25.txt

| | | | |
|------------------------|-------------------------|-------------------------|------|
| gtccacttct ccccgccctc | ctccttcgg tttccctcc | ctccctccca gtcaggctc | 3600 |
| agaggtgtgg tccccctccc | cctccaatgc cgccctccgt | ggcctcaccc tctccctgtc | 3660 |
| tcgttaggcct gtccttaggt | tcctccctcg cctataagct | ggctttaccc ctctctgtct | 3720 |
| tccaggcacc tgtggtctta | gchgctccct ctctctgaac | ctcgccccgt ggaaacttgt | 3780 |
| gcactgagct ctctcttctt | gtttgcttct ccctctcatc | acttgcttcc cggggccctg | 3840 |
| ccctgactgc tgcaccacca | ctcctgctct tgtgatctcc | agggctttct agatctccag | 3900 |
| gtccagcaaa tgcttttcag | cccttccttg cttgacatga | cgactttgtg acaaatttga | 3960 |
| ccagtccttc agtgacgctc | ttgcctcggc atttatgacc | tgccacccctt ctctcaacttg | 4020 |
| tggtacctcc ttctcagtct | cctttggaga atctccctccc | cccctcttct gaaaaagtgg | 4080 |
| atgattcccc gagtgccagga | ccactccctt tcccaggcag | gtgctggag caaacaactt | 4140 |
| tccctactct tcaagaatct | ttctggctgg tctaaaaata | agttgatgtg acacaganaa | 4200 |
| aaggaaaagt caaatcacgt | atgtacaggg anctacnaaa | cacgaaaggt caaganagga | 4260 |
| aangngaggct anctgctatc | tgaactatga acaagggnag | ggtaaaattc aaggaaagaa | 4320 |
| gaaatcanag aaagaagagg | nanggtataa aagntgctgg | ccatcaaaaaa tggaaaggaag | 4380 |
| aattanaann gattggagnn | nnnnnnnnnn nnnnnnnnnn | nnnnnnnnnn nnnnnnnnnn | 4440 |
| nnnnnnnnnn nnnnnnnctt | ttcccgtcac cggtggccag | ggttaaattc aggctgcca | 4500 |
| gctgtttttt gggatgactc | cagcagtctc cttagggagtt | cttcctgact ctggcttga | 4560 |
| gccttttcta acacattctt | cactgaaatc agatacaccc | ctgaaacaca agtctggca | 4620 |
| gattacctct ctgcctagac | attnaagggg ctccccaggg | cctgcagata aagaccaagt | 4680 |
| atcttagcta tcttggtgcc | aggagtaagg ctcctgccc | tgaccagaca cgccactt | 4740 |
| tgtgctcctt ctccggctt | ccaacctcct ggtcagttc | tctcaactggg ttagctttt | 4800 |
| gttcttttcc ctttcttctc | ccacaaacct cccccctgggt | ttctgcctct tcttttagatg | 4860 |
| tagctggtcg gcctcctagt | ccaccagagc tgcctttag | agccagggt gggaccatgt | 4920 |
| ctccctcctc ctcgggtccc | cgcgc当地 cagggccag | cacttggagg ctctgagtt | 4980 |
| aggccaaggc cactgaagtc | gctgaactga accccccccc | cggccccct ccgcagatca | 5040 |
| gctacgaggc cagcagcgtg | acgctcgag tgaagcggca | ttacccctcg tttctgcgca | 5100 |
| ccatccccag cgacaagcac | caggtggagg ccatggtgct | gctgctgcag agttcgggt | 5160 |
| gggtctggat ctccgggtgc | ggcagcgcacg gcgactacagg | gcagctgggg gtgcaggcgc | 5220 |
| tggaggagca ggcacccag | cagggcatct gcgttgcctt | caaggacatc atccccttct | 5280 |
| ctgcccggcc gggcgacgag | aggatgcaga gcatcatgca | ccacctggcc cgagcggagga | 5340 |
| ccaccgttgt ggtcgcccc | tccagcaggc agctggccag | ggtgttctt gagtcgggtgg | 5400 |
| tgctggccaa cctgactgcc | aaggtgtgga tcgcctcaga | agactgggcc atctctagac | 5460 |
| acatcagcaa tgtgccccgg | atccaggcga ttggcacgg | gctgggtgtg gccatccagc | 5520 |
| agaggcttgt ccctggcctg | aaggagttt aagaggccta | tgtccaggca gataaggggg | 5580 |
| ccccctggcc ttgctccagg | acctccgagt gcagcagcaa | ccagctctgt agagagtgc | 5640 |

MON-0301.ST25.txt

| | |
|---|------|
| gggcttcac ggcagagcag atgcccacgc tcggggcatt ctccatgagc tctgcttata | 5700 |
| acgccttaccg ggcagtctac gcagtggccc atggcctcca ccagctcctg ggctgtgcct | 5760 |
| ctggagcctg ttccaggac cgagcttacc cctggcaggt aaggtagccc agaccccgcc | 5820 |
| accctgaaac ggggtgcctt cctaaggcaa acagagtgtat ccctctctgg ccaactgagt | 5880 |
| gctgggggtg ggggacaaag gccacccatc agaaggctaa ttccctctct tgggcttcac | 5940 |
| ttctctgacc tcggcccctc ccaccacat gctccagacc cagggctaaa aatctctggg | 6000 |
| aaacgggcct ttttagaagc ttcccttcac tcaggaggcc agttgggagg gtcgaggggc | 6060 |
| ttccttgaa gggagggggc tctgaatttc cagacagact gaaaccaccc aaatagaagc | 6120 |
| atttgttcc taagcttcc gggtctggga gagttgagga ggagcagcct gcgtcatctg | 6180 |
| tggctgtcc atgatccccg tttatctcg cttctggagc agatccgcaa ggtgaatttc | 6240 |
| ctcctacaca aggacaccgt gaggttaat gacaacgggg accctctcg tggctacgac | 6300 |
| ataattgcct gggactggag tggcccaag tggacttca gggtcattgg ctccatcg | 6360 |
| tggcctccag ttcagctgga cataaataaa accaaaatcc ggtggcacgg gaaggacaac | 6420 |
| caggtaatgg agccatggtc actcaccaag tcaccgcctt acgggcagcc tggagcctga | 6480 |
| agtcaactgtc gacacagctc acacggagca ggagggggcc cgggtgccca ggccaacgtg | 6540 |
| gctctatcca gcccgtccag ggaagccccca cagaccgcac ccagatggcc ggctgcagct | 6600 |
| ggtatacaca accagggct gtgccttggg agtgagctgt gagggcagat gcacggagac | 6660 |
| tcccatcgc catgtgagca tcccttgact tggccactc catgtggttc cagaacacct | 6720 |
| gtggcttctt gcaggtgccaa aagtctgtgt gctccagcga ctgcctcgaa gggcaccagc | 6780 |
| gagtgatttc gggtttctac cactgttgct ttgagtgtgt gccctgtgag gccggagct | 6840 |
| tcctcaacaa gagcggtgag tgtccaaatg agtggagaa tgactggca ctcccagggt | 6900 |
| ctgtatggca gatgagggga tctcccttgg gccacgcac tgcaagaacca gagccttgct | 6960 |
| ccctctgttg ccagttgagg tacagggtgt agaatatttg ccaccagact gagttctgtat | 7020 |
| gaagcagaaa ccaacaacca gttgaaatcc tcaggtcccc tacgttttt actagaggc | 7080 |
| tcctgatgca atccctgcag atgcaatctt atcctaaatt caacctttt atgcgaacag | 7140 |
| atgttagttat gttcccttgc cccctccat gctgtctgtg tgaagtccct tccgtcgccc | 7200 |
| ctgccaaaga cagccagcac cttggacagc ttggccttga tgcaagatact attgtatccg | 7260 |
| cagacaagaa acatagcata ctccacccag tggatggcagca aggtcaagat cagagagcaa | 7320 |
| actcaggttag ctaagggctc agcccaagagc tggactctgt gagccacgtt ctccctttt | 7380 |
| actatctctg tggcggtgag aacacatctc ttctgttctc agagagtcag agaaaccaca | 7440 |
| gaatggcagc acagataggg ggctttgggt aatggaaagcg ctggggagat gaaaatgccc | 7500 |
| ttcccttggg gctgggtgct cctgttggat catgcctca ctggcatgtg ggcagagcta | 7560 |
| ccagagtaag gcccctctca aggatctctc ggtttgcaag cccctctgg gatcataagc | 7620 |
| catacagaac ctacccaagg gtctccagaa tctgcaatta acacaggcat ctggaggaaa | 7680 |
| cacttggccg cggggccccca ctcagggcta ccccttatct cgctgtgtgc agtaggagcc | 7740 |

MON-0301.ST25.txt

| | | | | | | |
|-------------|-------------|-------------|-------------|-------------|------------|------|
| cggcttctgg | ggtacagcgc | tcccagcacc | ttgcaggcct | acatggcttc | ccttcctcat | 7800 |
| tcctgtctgt | ctcatctagg | ctctcaggag | ccccctccac | cttttcttc | cagacctcca | 7860 |
| cagctgccag | ccttgtggga | aagaagagtg | ggcaccccgcg | ggaagtgaaa | cctgctttcc | 7920 |
| acgcaccgtg | gtgttttgta | cttggcacga | gaccatctct | tgggtgctgc | tggcagctaa | 7980 |
| tacgttgctg | ctgctgctgg | tgactggac | tgctggcctg | tttgcctggc | acttagacac | 8040 |
| ccctgtggtg | aagtccgctg | ggggccgact | gtgcttcttc | atgctaggct | ccctggcagg | 8100 |
| gggcagctgt | gggcctctacg | gcttttttgg | ggagccacag | ctgcccacat | gcttgttgcg | 8160 |
| ccaaaggcctc | cttgccttgg | gttttgccat | cttcctgtcc | tgcctgacca | tccgctcctt | 8220 |
| ccaactggtc | ttcatcttca | agttttctgc | caaggtaccc | actttctacc | gtgcctgggt | 8280 |
| ccaaaaccac | ggtcctggcc | tattttgtgt | gatcagctca | atggcccaagc | tgctcatctg | 8340 |
| tctaacttgg | ctggcggtgt | ggacccact | gccaccagg | gagtaccagg | gcttccctca | 8400 |
| gctggtgtg | cttgatttgc | cagaggccaa | ctcaccgggc | ttcatgttgg | ctttgcctta | 8460 |
| caatggcctc | ctgtccgtca | gcgccttgc | ctgcagctac | ctgggcaagg | acgtgccaga | 8520 |
| gaactacaac | gaggccaaat | gtgtcacttt | tagtctgctg | ctcaacttcg | tgtcctggat | 8580 |
| tgccttcttc | accacggcca | gcgtctacca | ggcaagttac | ttgcccgcgg | tcaacgtgct | 8640 |
| ggcggcgctg | agcagcctga | gtggcggctt | cagcggttat | ttcctcccca | agtgtacgt | 8700 |
| gatcctgtgc | cgtccaaaat | ttaacagcac | acagcacttc | caggcctcca | tccaggagta | 8760 |
| cacgaggcgc | tgcggctcca | cctgaccagt | ggggcgggca | gggcctagcc | ggggaggtgg | 8820 |
| ggggtggggg | gtgaagggggt | agaaggtggg | gtaggggcgc | ctcccctgcc | ctgagggtcg | 8880 |
| aagggtcgagc | gaggcgagcg | ggcccccgcgc | cctccgggag | gccttttgg | ctcctgtctt | 8940 |
| ggctcgggta | gtgtacgctc | acgggagtcc | agtccaggct | ccgagctgcc | aataaagcgg | 9000 |
| tgaaacatgc | gtcctggctg | ctctagctgt | ctgaaccgag | ggtggggcg | | 9049 |

<210> 60
<211> 2526
<212> DNA
<213> Felis catus

| | | | | | | |
|------------|-------------|------------|------------|-------------|------------|-----|
| <400> 60 | | | | | | |
| atgtcactcc | cggcggctca | cctggtcggc | ctgcagctct | ccctctcctg | ctgctgggct | 60 |
| ctcagctgcc | acagcacaga | gacgtctgcc | gacttcagcc | tccctgggga | ttacctcctc | 120 |
| gcaggtctgt | tccctctgca | ctctgactgt | ccgggcgtga | ggcacccggcc | cacggtgacc | 180 |
| ctctgtgaca | ggcccgacag | cttcaacgg | cacggctacc | acctcttcca | ggcoatgcgg | 240 |
| tttggcatcg | aggagataaa | caactccacg | gccctcctgc | cgaacgtcac | cctggatac | 300 |
| cagctgtacg | acgtgtgctc | ggagtctgcc | aacgtgtatg | ccacactaaa | cgtgtctcc | 360 |
| ctgctgggga | cacatcacgt | agagatccga | gcagaccctt | cccactattc | gcctgcccgg | 420 |
| ctggctgtca | ttgggcctga | caccaccaac | cacgcagcca | ccactgcagc | cctgctgagc | 480 |
| cccttcctgg | tgcccccgtat | cagctacgag | gccagcagcg | tgacgctcgg | agtgaagcgg | 540 |
| cattaccct | cgtttctgctg | caccatcccc | agcgacaagc | accaggtgga | ggccatgggt | 600 |

MON-0301.ST25.txt

| | |
|--|------|
| ctgctgctgc agagcttcgg gtgggtctgg atctcggtgg tcggcagcga cggcgactac | 660 |
| gggcagctgg gggtgccaggc gctggaggag caggccaccc agcagggcat ctgcgttgcc | 720 |
| ttcaaggaca tcatccccctt ctctgcccgg ccgggcgacg agaggatgca gagcatcatg | 780 |
| caccacctgg cccgagcgg gaccaccgtt gtggtcgttt tctccagcag gcagctggcc | 840 |
| agggtgttct ttgagtcggt ggtgctggcc aacctgactg ccaagggtgtg gatgcctca | 900 |
| gaagactggg ccatctctag acacatcagc aatgtgccccg ggatccaggc cattggcacg | 960 |
| gtgctgggtg tggccatcca gcagaggctt gtccctggcc tgaaggagtt tgaagaggcc | 1020 |
| tatgtccagg cagataaggg ggccctggg cttgtccca ggacctccga gtgcagcagc | 1080 |
| aaccagctct gtagagagtg tcgggctttc acggcagagc agatgccac gctggggca | 1140 |
| ttctccatga gctctgctta taacgcctac cgggcagtct acgcagtggc ccatggcctc | 1200 |
| caccagctcc tgggctgtgc ctctggagcc tggccagg accgagtcta cccctggcag | 1260 |
| cttctggagc agatccgcaa ggtgaatttc ctccctacaca aggacaccgt gaggttaat | 1320 |
| gacaacgggg accctctcag tggctacgac ataattgcct gggactggag tggccccaag | 1380 |
| tggaaacttca gggtcattgg ctccctccatg tggcctccag ttcaagctgga cataaataaa | 1440 |
| accaaaaatcc ggtggcacgg gaaggacaac caggtgccaa agtctgtgtg ctccagcag | 1500 |
| tgcctcgaag ggcaccagcg agtgatttcg ggtttctacc actgttgc ttcaagctg | 1560 |
| ccctgtgagg cccggagctt cctcaacaag agcgacccctc acagctgcca gccttgtgg | 1620 |
| aaagaaaaagt gggcacccgc gggaaagtcaa acctgctttc cacgcaccgt ggtgttttg | 1680 |
| acttggcacg agaccatctc ttgggtgctg ctggcagcta atacgttgc gctgtgtgc | 1740 |
| gtgactggga ctgctggcct gtttgcctgg cacttagaca cccctgtggt gaagtccgct | 1800 |
| ggggccgac tgtgcttctt catgctaggc tccctggcag gggcagctg tggctctac | 1860 |
| ggcttttttg gggagccac gctgcccaca tgcttgtgc gccaaagcct cttgcctcg | 1920 |
| gttttgcca tcttcctgtc ctgcctgacc atccgctcct tccaaactggt ctcatcttc | 1980 |
| aagttttctg ccaaggtacc caccttctac cgtgcctggg tccaaaacca cggtcctggc | 2040 |
| ctatttgtgg tgatcagctc aatggccag ctgctcatct gtctaacttg gctggcggtg | 2100 |
| tggacccac tgcccaccag ggagtaccag cgctccctc agctgggtgt gcttgattgc | 2160 |
| acagaggcca actcaccggg cttcatgttg gctttcgccct acaatggcct cctgtccgctc | 2220 |
| agcgcctttg cctgcagcta cctggcaag gacctgccag agaactacaa cgaggccaaa | 2280 |
| tgtgtcactt ttagtctgct gctcaacttc gtgtcctggta ttgccttctt caccacggcc | 2340 |
| agcgtctacc agggcaagta cttgcccgcg gtcacacgtgc tggccgcgt gagcagcgt | 2400 |
| agtggcggct tcagcggta tttccctcccc aagtgtacg tgatcctgtg ccgccccaaaa | 2460 |
| tttaacagca cacagcactt ccaggcctcc atccaggagt acacgaggcg ctgcggctcc | 2520 |
| acctga | 2526 |

<210> 61
 <211> 841

MON-0301.ST25.txt

<212> PRT
<213> Felis catus

<400> 61

Met Ser Leu Pro Ala Ala His Leu Val Gly Leu Gln Leu Ser Leu Ser
1 5 10 15

Cys Cys Trp Ala Leu Ser Cys His Ser Thr Glu Thr Ser Ala Asp Phe
20 25 30

Ser Leu Pro Gly Asp Tyr Leu Leu Ala Gly Leu Phe Pro Leu His Ser
35 40 45

Asp Cys Pro Gly Val Arg His Arg Pro Thr Val Thr Leu Cys Asp Arg
50 55 60

Pro Asp Ser Phe Asn Gly His Gly Tyr His Leu Phe Gln Ala Met Arg
65 70 75 80

Phe Gly Ile Glu Glu Ile Asn Asn Ser Thr Ala Leu Leu Pro Asn Val
85 90 95

Thr Leu Gly Tyr Gln Leu Tyr Asp Val Cys Ser Glu Ser Ala Asn Val
100 105 110

Tyr Ala Thr Leu Asn Val Leu Ser Leu Leu Gly Thr His His Val Glu
115 120 125

Ile Arg Ala Asp Pro Ser His Tyr Ser Pro Ala Ala Leu Ala Val Ile
130 135 140

Gly Pro Asp Thr Thr Asn His Ala Ala Thr Thr Ala Ala Leu Leu Ser
145 150 155 160

Pro Phe Leu Val Pro Leu Ile Ser Tyr Glu Ala Ser Ser Val Thr Leu
165 170 175

Gly Val Lys Arg His Tyr Pro Ser Phe Leu Arg Thr Ile Pro Ser Asp
180 185 190

Lys His Gln Val Glu Ala Met Val Leu Leu Leu Gln Ser Phe Gly Trp
195 200 205

Val Trp Ile Ser Val Val Gly Ser Asp Gly Asp Tyr Gly Gln Leu Gly
210 215 220

Val Gln Ala Leu Glu Glu Gln Ala Thr Gln Gln Gly Ile Cys Val Ala
225 230 235 240

Phe Lys Asp Ile Ile Pro Phe Ser Ala Arg Pro Gly Asp Glu Arg Met
245 250 255

Gln Ser Ile Met His His Leu Ala Arg Ala Arg Thr Thr Val Val Val

MON-0301.ST25.txt
260 265 270

Val Phe Ser Ser Arg Gln Leu Ala Arg Val Phe Phe Glu Ser Val Val
275 280 285

Leu Ala Asn Leu Thr Ala Lys Val Trp Ile Ala Ser Glu Asp Trp Ala
290 295 300

Ile Ser Arg His Ile Ser Asn Val Pro Gly Ile Gln Gly Ile Gly Thr
305 310 315 320

Val Leu Gly Val Ala Ile Gln Gln Arg Leu Val Pro Gly Leu Lys Glu
325 330 335

Phe Glu Glu Ala Tyr Val Gln Ala Asp Lys Gly Ala Pro Gly Pro Cys
340 345 350

Ser Arg Thr Ser Glu Cys Ser Ser Asn Gln Leu Cys Arg Glu Cys Arg
355 360 365

Ala Phe Thr Ala Glu Gln Met Pro Thr Leu Gly Ala Phe Ser Met Ser
370 375 380

Ser Ala Tyr Asn Ala Tyr Arg Ala Val Tyr Ala Val Ala His Gly Leu
385 390 395 400

His Gln Leu Leu Gly Cys Ala Ser Gly Ala Cys Ser Arg Asp Arg Val
405 410 415

Tyr Pro Trp Gln Leu Glu Gln Ile Arg Lys Val Asn Phe Leu Leu
420 425 430

His Lys Asp Thr Val Arg Phe Asn Asp Asn Gly Asp Pro Leu Ser Gly
435 440 445

Tyr Asp Ile Ile Ala Trp Asp Trp Ser Gly Pro Lys Trp Asn Phe Arg
450 455 460

Val Ile Gly Ser Ser Met Trp Pro Pro Val Gln Leu Asp Ile Asn Lys
465 470 475 480

Thr Lys Ile Arg Trp His Gly Lys Asp Asn Gln Val Pro Lys Ser Val
485 490 495

Cys Ser Ser Asp Cys Leu Glu Gly His Gln Arg Val Ile Ser Gly Phe
500 505 510

Tyr His Cys Cys Phe Glu Cys Val Pro Cys Glu Ala Gly Ser Phe Leu
515 520 525

Asn Lys Ser Asp Leu His Ser Cys Gln Pro Cys Gly Lys Glu Lys Trp
530 535 540

MON-0301.ST25.txt

Ala Pro Ala Gly Ser Glu Thr Cys Phe Pro Arg Thr Val Val Phe Leu
545 550 555 560

Thr Trp His Glu Thr Ile Ser Trp Val Leu Leu Ala Ala Asn Thr Leu
565 570 575

Leu Leu Leu Val Thr Gly Thr Ala Gly Leu Phe Ala Trp His Leu
580 585 590

Asp Thr Pro Val Val Lys Ser Ala Gly Gly Arg Leu Cys Phe Phe Met
595 600 605

Leu Gly Ser Leu Ala Gly Gly Ser Cys Gly Leu Tyr Gly Phe Phe Gly
610 615 620

Glu Pro Thr Leu Pro Thr Cys Leu Leu Arg Gln Ser Leu Leu Ala Leu
625 630 635 640

Gly Phe Ala Ile Phe Leu Ser Cys Leu Thr Ile Arg Ser Phe Gln Leu
645 650 655

Val Phe Ile Phe Lys Phe Ser Ala Lys Val Pro Thr Phe Tyr Arg Ala
660 665 670

Trp Val Gln Asn His Gly Pro Gly Leu Phe Val Val Ile Ser Ser Met
675 680 685

Ala Gln Leu Leu Ile Cys Leu Thr Trp Leu Ala Val Trp Thr Pro Leu
690 695 700

Pro Thr Arg Glu Tyr Gln Arg Phe Pro Gln Leu Val Val Leu Asp Cys
705 710 715 720

Thr Glu Ala Asn Ser Pro Gly Phe Met Leu Ala Phe Ala Tyr Asn Gly
725 730 735

Leu Leu Ser Val Ser Ala Phe Ala Cys Ser Tyr Leu Gly Lys Asp Leu
740 745 750

Pro Glu Asn Tyr Asn Glu Ala Lys Cys Val Thr Phe Ser Leu Leu Leu
755 760 765

Asn Phe Val Ser Trp Ile Ala Phe Phe Thr Thr Ala Ser Val Tyr Gln
770 775 780

Gly Lys Tyr Leu Pro Ala Val Asn Val Leu Ala Ala Leu Ser Ser Leu
785 790 795 800

Ser Gly Gly Phe Ser Gly Tyr Phe Leu Pro Lys Cys Tyr Val Ile Leu
805 810 815

Cys Arg Pro Lys Phe Asn Ser Thr Gln His Phe Gln Ala Ser Ile Gln

820 825 MON-0301.ST25.txt 830

Glu Tyr Thr Arg Arg Cys Gly Ser Thr
835 840

<210> 62
<211> 10607
<212> DNA
<213> Felis catus

<220>
<221> misc_feature
<222> (1604)..(1683)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (2470)..(2516)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (2537)..(2537)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (2560)..(2560)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (2574)..(2574)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (2580)..(2580)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (2599)..(2599)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (2850)..(2850)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (5784)..(5830)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (7512)..(7553)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (8626)..(8626)
<223> n is a, c, g, or t

<220>
<221> misc_feature

MON-0301.ST25.txt

```

<222>  (10453)..(10453)
<223>  n is a, c, g, or t

<220>
<221>  misc_feature
<222>  (10491)..(10491)
<223>  n is a, c, g, or t

<220>
<221>  misc_feature
<222>  (10501)..(10501)
<223>  n is a, c, g, or t

<220>
<221>  misc_feature
<222>  (10511)..(10511)
<223>  n is a, c, g, or t

<220>
<221>  misc_feature
<222>  (10545)..(10545)
<223>  n is a, c, g, or t

<220>
<221>  misc feature
<222>  (10558)..(10558)
<223>  n is a, c, g, or t

<220>
<221>  misc_feature
<222>  (10574)..(10574)
<223>  n is a, c, g, or t

<220>
<221>  misc_feature
<222>  (10599)..(10599)
<223>  n is a, c, g, or t

<400>  62
ttagctgctg aaacgctgct ttttagcaaa aggccgtgac ctcatgatgt tatacgtcg 60
ggagattgag aaccagggtcc tagcatctga ctatgtgctt tgagtccccca ctttgctgg 120
ttgtgcaacc cagggtgagc ttcgtaagct tctctgtgcc tcagtttct catctgtgga 180
atggggccgg tcatagtccc cgttattgtg atcatcgagc aagatggtga atggcgagca 240
cacagcatga tgcctagttc ttactggaac acctgtcctg ggtcaggggc tgtatataaa 300
gtactacctg ccaggatcaa cttgatccgg ttctattctg tctctctgggt gagtatctgt 360
gccctttact cccagatgtt ggaaatgtca ggggcatgag acctgtcctt aaccgagtgg 420
cagaaggta agtttgtgtc cgagatagca ggacatgctt tctctacctc cgcaggcgt 480
tctccagac cccccagggc ccaccatgcc ctgctaggaa gggatcatcc taattctagc 540
ctcttcttcc gccccagagt tctgaagctt ctccacctgt ccaggtgttt ccccacccct 600
tcagccacgg caagaccgtc actatgtaaa tgtctgtgca aatccctgg tgtcaagctg 660
ccagctctct gatgaggcag gcccacctcc ggggacccct cacttcccag ccatgggacc 720
ccggggccagg gaagtctgct gcttcatcat cctgcccgg ctccctggctg agccggctga 780
gaactcagac ttctacttgg ctggggatta ctccctcgcc ggcctttca ccctccatgc 840
caacgtgaag ggcacatcggtcc acctaaccct cctgcaggtg ccccagtgca aggagtgagt 900
cgccaatgtg gggctggaag tggcgacggg ggcggagtg 960

```

MON-0301.ST25.txt

| | | | |
|------------------------|------------------------|-------------------------|------|
| gctcctcagg ggaccacgcc | aggaccaagg gctcaaaatg | ctcttcctca ttcattgcca | 1020 |
| acctctcatc ccgcattatc | cccaccggcc tgcagggaga | ccccatgcag ttcatgttac | 1080 |
| caaaaatctt ggcaattgtt | ttctgaaata tggagagctg | gttgtccgc cgtgtgtctt | 1140 |
| aataaataaa gagttacagg | gtacttgagc ctggaggggt | tgttagagacc accccccac | 1200 |
| actttgtcaa gtggggaaact | cctactgagt ccgtgtcaag | tccaagtcta gacaccgggg | 1260 |
| gttatgcctt tggaggcgag | aatgtggtt ttcggtagc | aggttctcag actggagggg | 1320 |
| aagggttgca tttctctagg | gctgtggta ggtggaaagg | ggtgcttcca ggaccagaag | 1380 |
| ggatttcctc cactcacctt | gtccccgtg agccctgggg | gtggctgcat cactcaaggt | 1440 |
| tgggtgagac acctttgtgc | aagtgcgaag gctggatgg | cggaccacgc gtggatgat | 1500 |
| gagatagtga ctgcgtgcag | agagggtgaa ggcgtcctgt | gagagagggg gaaaaaaag | 1560 |
| tctgtgacgt cggggaaagat | cacatgctgg ctgagaatg | acgnnnnnnn nnnnnnnnnn | 1620 |
| nnnnnnnnnn nnnnnnnnnn | nnnnnnnnnn nnnnnnnnnn | nnnnnnnnnn nnnnnnnnnn | 1680 |
| nnngatgtgg aggtgatrgt | gatggcggtg attgtgacgg | tggtatcggt gatgggtggc | 1740 |
| acagacaacg cagttatagt | gatggcagtg gtgataggaa | tagtaggtgg tcatgggtcat | 1800 |
| tctggagatg tggcaggtga | caacgatgag atgaaaatgc | cagaatcttc tggagtggct | 1860 |
| ccttccttgcg ccactcctcg | gctttcctat ggcaggcaga | ggggactccc cggctctcct | 1920 |
| gtcccttccc cctctactc | tggacctgcc tctcacccca | ccccacatgg ctcccccagg | 1980 |
| tatgaaataa aggtgttggg | ctacgatctc atgcaggcca | tgtgcattgc aggggaggag | 2040 |
| atcaatagcc agagcagcct | gctgcctggc gtgctgctgg | gctacaaaat ggtggatgtc | 2100 |
| agctacatct ccaacaatgt | ccagccctgt ctccacttcc | cggcaaagga ggactgttcc | 2160 |
| ttgcccattcc aggaggacta | cagccactgt gtgccccgtg | tggtggtgtt cattggcct | 2220 |
| ggcaactctg agtccactgt | gactgtggcc cgcttcctct | ctcttcctt cttccacag | 2280 |
| gggaggcccc tgggtcctgg | ggttaaggagc tggggggcag | aggagtggtt atccaggggg | 2340 |
| ctcacttccc cccaccggtc | ctggggtag gaggaggcag | gaagtaggggt cagaatgtca | 2400 |
| accccaatcc trggaggca | gcccagccac gtggtaaga | gctcaggctt ggaggcagac | 2460 |
| agacckgggn nnnnnnnnnn | nnnnnnnnnn nnnnnnnnnn | nnnnnnnnnn nnnnnngcct | 2520 |
| tcagagagat catccntca | agggggccct tattcctttn | ccctggag cccntcagtn | 2580 |
| cccaccactt tctgcagcnc | ccattcgggt ctccgattcc | tccaaatccac tcactcgctg | 2640 |
| tgtggctctg gataagtgac | tgtccctctc tgaacctcag | cgtcctcatc tgcaaagtgg | 2700 |
| agacataaca gcacatcaga | aggtcgcgag aatagggcgc | cctggggaggc tcagtcgggt | 2760 |
| aagcatccga ttctgggtcg | cggctcaggt catgatctcc | cggttcgtga gttcaagccc | 2820 |
| cgcacatggc tgggtgtctg | cagcacagan cctgcttggg | attctgtctt ccctctctc | 2880 |
| tgcccctcac ctgcctttgc | tctctctctc taaaataaa | taaataaaact ttttaaaaaaa | 2940 |
| aaggaaggta gtgagaaaaaa | agcgggtgac agagatggag | agggctccac gcggtacctg | 3000 |
| gcatgctgca gcccctcaga | accggttagc gacggaaagtg | acctgtgtgc gtcgtcacca | 3060 |

MON-0301.ST25.txt

| | |
|---|------|
| ccatcccagc aggccctttag gcttcgaccc tgccctcccc gcaaagctca cagtctccga | 3120 |
| ggctccgggc cacgtcccc gggcgctctg tctgtgtccc tcgaaccccg cccagccctg | 3180 |
| ccgcaccgtg agctagtcag cgccctgtgg gttcgtact ctctccgcca ttgtgcaccc | 3240 |
| tggggctggg gccacaccca ggggctccgg ttaatttaga tgctttctt ctctgccatc | 3300 |
| tgcttacccc cgagcttgggt tagagagcct gactttgctg ggagtctcca gaacgtcccg | 3360 |
| ggacctccca gcaaccagca tctttattct ccctccttag aactgatgtg tgcatcgct | 3420 |
| gtgcctctgc agctcagagc aggggtgggt cctgtgaact gggccaggg gtggtttcct | 3480 |
| ggagggggca aggcaccgac tagccctcga agaaggagcc gggcttgct gaggtggac | 3540 |
| agggggagag catgagggtt tcggccagct ttctgtgcct gggAACCCCC tctccccaca | 3600 |
| accctggatc ccagaggcct taacggccc cagctgtaac agactcgct gtgtcgagca | 3660 |
| ttccacagta ggtgtccccca ggctccctcg gggccaccaa aggaccacaa cgacattacg | 3720 |
| cggacagggt ctcagattcc gatgggtccc ctgtttgctg gaaccatctc cctttggaaa | 3780 |
| tttacagctc tctttctgg cagtaacccc gccccttggt gctgggtacg aagggggcac | 3840 |
| ccagagcggg gctcacccag cagcgctgac tgctgcgttg tcgggctaac gggtattaac | 3900 |
| cgcctccctc gccgctccca ttctcttagc tgctgaaacg ctgctttta gcaaaggccg | 3960 |
| tgacctcatg atgttatacg tcgtggagat tgagaaccag gtcctagcat ctgactatgt | 4020 |
| gctttgagtc cccacttttgc tggttgtgc aaccctgggt gagcttcgta agcttctctg | 4080 |
| tgcctcagtt ttctcatctg tggaatgtgt gagggggaga ctcagtttc aagcggggtg | 4140 |
| gccaggaggg ccttctgac aactggacaa cgacctgagg gagaggaagg agtgagggag | 4200 |
| ctatgtgggt gcctagaaga ggcgtccgga agagggggca gcaaatgcag aggccggcag | 4260 |
| gagcctggtg cggtggctga accggtgagc agccccggga ccaggcggga cagtaggaga | 4320 |
| agatgaagcc agagagggtga gggccggggt cagtggtgga gccccttggg ggccactgaa | 4380 |
| ggactctggc tgcctcgag tgacattagg agctgttggg gagttttgag ctgaggagta | 4440 |
| aggtgacgga caagtggtcg cagaggccac cggctgcca cgaacagcag cagagacagc | 4500 |
| caaggggaag ggtggggggc tgtggtgacc cggggagggt ggtgatggtg gcccggtgag | 4560 |
| gccctagctc acgctggcgg ccctccgctc tccggcagat cacctacagc gccatcagtg | 4620 |
| acgagctacg ggacaagcag cgcttcccg ccctctgac cacagcggcc ggcgccgatc | 4680 |
| accagatcga ggcctatggtg cagctgatgt tgtacttccg ccggaaactgg atcatcgcc | 4740 |
| tggtgagcag cggcgactgc ggcgcgacg acagccagct gtcagcgtat cgcggccgg | 4800 |
| gcggcgacac ctgcattcgcc ttccggaga cgcgtcccat gccccagccc aaccaggcgg | 4860 |
| tgacgcagtgc ggagcggccgg cgcctgaagg ccatcgtgga cgagcagcag cggcagagct | 4920 |
| ctgcgcgcgt cgtggctctg ctgtcgccaa agctggctt gcacaacttc ttccgcgagg | 4980 |
| tgctccgcca gaacctcact ggcgtcgtgc ggatcgccctc cgagtcctgg gccatcgacc | 5040 |
| cggcctgca cgacaggccc acgctgca cgcctcctg ggctgcaccc agaccagcag | 5100 |
| ctccgggtcg tctatccctg gcaggtgagg ccccacccac ggagagtcgg ggccacacac | 5160 |

| | |
|---|------|
| gcaggcgccg ccacagccct gagtggttgc catggagacc actgccctgc tctagcgtcc | 5220 |
| ccctctctgg cgggtcctg ggcaaactgg cggagagggc cagggacgt accctgtccc | 5280 |
| cagacacata aagccagaag tgcttcatgg tgacaaaact cctttttta cattaatgtta | 5340 |
| atcctcgcca tccaagatag cctgtccgg caggagattt gggtaagtt tccttggagg | 5400 |
| aggcctggca ggcagtggc cccctggcc ccctgccgtt tctccagggt ggcggccttgc | 5460 |
| ggggaggact tctgtgttca gctctctgag gctctgcctt gggtttatgc atcttctctc | 5520 |
| gtcccaggtc tggacgattc agaggagtaa ggaggcaagg agtcgcctgg attcagaccc | 5580 |
| ggaatttaaa tctgtatTTT tctgatctgc gtgcacacccc gcgcgtgcac acacacacac | 5640 |
| ctaaccacga agtttatgtta ggtagaagat ttactgagg gggcgcctgg gtggctcagt | 5700 |
| cggtaagcg tccgacttca gccaggtcac gatctcgccg tctgtgagtt cgagccccgc | 5760 |
| gtcaggctct gggctgatgg ctcccccccc nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn | 5820 |
| nnnnnnnnnnn agcaccccgaa gggccggggg gagggcacct gagccgtaa agggaaacag | 5880 |
| gagtggcctc tgaacccagg tgataggctc ccgctggatg gcagacgtga ctccacggg | 5940 |
| agcaggaata atgtcgacac atcggccgga aggggagcac ttccctgggtgc gcagtcatttgc | 6000 |
| tgctaagctc ccaacattgg gaaactcatg cgttgcttca gagccggga gacagggttt | 6060 |
| tttgtgtcct actttacaga agaggagact ggagctcacg ggggttgggc gacaggcccc | 6120 |
| aggctcagag caggtggcag agctggtgc tgaacccagg tgtgtctgac tacagagccg | 6180 |
| gggctccag ccgctgcctc ccgggtgacc acatctgcgg tctcattgcc cccttggtagg | 6240 |
| gatgtggaca cccagtctcg tgggttagtc actctcccc ggatcgagcc cgacttcttt | 6300 |
| ttttttttttt aaaaaaaaaa tcaacgttta ttatTTTggacagagag agacagagca | 6360 |
| tgaatggcg agggcgagag agagagggag acacagaatc ggaaacaggc tccaggctcc | 6420 |
| gagccatca gccagagcct gatcgaaaaa tcaactcac ggaccgcgag atcgtgaccc | 6480 |
| ggctgaagtc ggacacttac ccgaatgcgc caccagggg cccagatcga gcccacttc | 6540 |
| tgacgcccagc gtcgcttcct ttccctgtgg cctccagct gcttcaggaa atctggagg | 6600 |
| tcaacttcac cctcctggc caccagatct tttttgc gcgagggggac ctactcatgc | 6660 |
| gcctggagat catccaggga cgggtggacc tgagccagaa ctttctggc gcgtgcctc | 6720 |
| ctactgccccg gtgctacgac ggctgaggc catccgtgac gtatctggc acacggccaa | 6780 |
| caacacggtc agctctcgga gggctggtgg gggctggga ctttctggc ggcactggct | 6840 |
| cgtgcagggg tggcaaggc cctgtggacc tgagatccat tatcgagcac tgatgtcatc | 6900 |
| cctatttgc ggtgtccctc ctccccattga ctaagcactg tggaagtcta gagctttctg | 6960 |
| gatcctcagg acccaggggc tcagggggct gcacaaagtgc aacgttaggt ggacacgtgt | 7020 |
| gtgctaagga cttcaatttc catgtcaacc ctagggaaata gagagtaactg ttccctctgt | 7080 |
| ctttggggtt gggaaaactgg aggacacagag ggggtcggt gaccataaaa aggccacaca | 7140 |
| gctttcgcat gtctctatac acagcattca gtctacatcc catcgattag tactcgcgtt | 7200 |
| ttggggacag tagctgtgcc ttcacctgtg tctgacatct gtcagtctga aagctccccc | 7260 |

| | |
|---|------|
| gttttaccct cttagcttac aagctgtcag aatggccgcg atgtggggaa ggttagagact | 7320 |
| cagcctcgtg gggaaaggggg gaggtgggg gacctaagat ttcaaagagc cagggcacct | 7380 |
| gggtggctca gtcagttaag catccgactc tggatctcag ctcagtcatt atctcaggtc | 7440 |
| gtgagtttag acccctgtgt agggctccgt gctgggcgcg cagcctactt aaaaataata | 7500 |
| aaaacaaaag cnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnngatcccc | 7560 |
| gtgtccatgt gttccaagga ctgccagct gggcaaagga agaagcccgt gggattcat | 7620 |
| ccctgctgct tcgagtgtct cgactgcctt ccggcacct tcctcaacca aactgcagat | 7680 |
| gggactcaca gacccacacc cctgccctgc cctgccctgc cccgccctgg ggctcccagg | 7740 |
| gcccttcatc tttggcaggg tctctggagt ctcatccagg ggacacaggt gtccaaaggc | 7800 |
| cagggaccat gtttgactc cgcttgtatc tccctaaccg ctggtgtaag aaaaatcttc | 7860 |
| aatgctgtga gggcgtgggg gtgggagaag gaacagccct caaccaggcg aggctgtaac | 7920 |
| tgatccctc tgacacacaca ttagctgag ggcccagggg ggtcaggcca gagaatgtcc | 7980 |
| accggatgaa cgaacgaatg aatgaatgaa cgaacgaaca aacacacaaa tgaatgaatg | 8040 |
| tctctgtccg tagaagaaat gtttctggca gacaggctta ggatctaatt tctctgtgt | 8100 |
| gcctcccgag tgctcgtgt agttcggagc atataatgtt tgctcagtga atgtttattt | 8160 |
| agtgacatcc ttgatgagaa gaattgacat ctccccstat agatcataaa ctccaggaaa | 8220 |
| ggggggacaa tgtcatccct ccagtgttta ccacagttca ccgttggggc cgaattattt | 8280 |
| tttttcatg acttcacaga ttagtaacta agcggttctg tacatctacc gatcagagta | 8340 |
| cttacgacgt gcccagcaga gcccaggcga caggtaggt gctcaacaaa agtttgttt | 8400 |
| caattgatca gtagccggaa gtcagggggc tcggtttat ccacgtctgt gctctccatc | 8460 |
| tcagatgcct atcacagtgg gtggcgctca aaaagaaaact tgaataaacg gtcgaatgtc | 8520 |
| catctcacca gagggtacgg tcttggaaagg gaggcattac gggtgccagg ctctgagtca | 8580 |
| aggggacctt ggaccacatc ctgcctctgt aactggttt gtaacngcct ggaggagcct | 8640 |
| cagatgccac atctgtgaaa tggggttgca gtgaggatct gatggccgg tggatacgg | 8700 |
| ggacgcagtg agaggtgcta cgaccgcagg catccctt ggctcgcccc ctccctaccc | 8760 |
| ctacagccgg ccgggtgcag gtgcagagga tgtgggtgcc gggaaagggtgg gtgtatctga | 8820 |
| tggaactgct gtgggctt gcagacgagt ttggctgccg gccctgcccc agttgcgggt | 8880 |
| ggtcccgag gaacgacgct tcgtgcttca agcggcggct ggcctccctt gaatgacgct | 8940 |
| aggcacccgc cgtcgctgtg gccgtgtgtt ccacccctggg ctccctctgc accctggcca | 9000 |
| tcctgggtat cttctggagg caccgcacg cgcccatgtt tcgctcgcc gggggccccca | 9060 |
| ggtgcttccc gatgccatg cccctgtgtt ataggtgacg gtctccatgt acatgggca | 9120 |
| gcccgcgtt ttcatgtgcc tcggccacca gaccctcttc accctctgt tcaccgtctg | 9180 |
| tatctccctgt gtcaccgtgc gcttttcca gatcgccgc gtcttcaaca tggccaggcg | 9240 |
| cctcccgctt gcctacggct actgggtccg ctaccacggg ccctgtgtct tcgtggcg | 9300 |
| cttcacggtg ctcaagatgg tcatcggtgc gggcaacgtg ctggccgcga cggccgagcc | 9360 |

MON-0301.ST25.txt

| | | | | | | |
|------------|------------|------------|------------|-------------|-------------|-------|
| cgccgcggc | cccggccccg | atgacccaa | gatcgcggtt | ctcgccctgca | actaccacaa | 9420 |
| cgtgctcctg | ttcgacacca | gcctggaccc | gcttctgtcc | gtggcgggct | tcggcttcgc | 9480 |
| ctacgtggc | aaggagctgc | ccaccaccca | caacgaggcc | aagtcttca | ccttccgcac | 9540 |
| gacccitcac | ttcaccttct | ccatctccct | ctgtaccttc | atgtctgtct | acgaggggg | 9600 |
| cctggtcacc | atcctgcacc | tcgtggtggc | agtgctcaac | cttctggg | cttggcccc | 9660 |
| tgggctactt | cggcccaag | tgctgcgtgg | tcctttctta | cccgatcac | aacacgccc | 9720 |
| tctacttcag | cagcatgatt | cagggctaca | ccaccggaa | ggacttagcac | tgccccctgg | 9780 |
| ctgcccaggg | ggccagaggg | ctcggtactg | ggagatggag | accaggggtg | gggctgggg | 9840 |
| tggtgtgac | tcattcagcc | cctgctggga | gcagggacac | cacccgc | tactctga | 9900 |
| tttggctcc | ccctccaggt | tctctgcacc | ctggccgttt | ttacccaccc | gctggtggat | 9960 |
| gcctaaaaat | acgcttccc | tgcagccgtt | tggcttgcca | ggcactgcca | cccatgctag | 10020 |
| ggaaaggagc | cgggtgacc | tccctatggg | tctccaagac | agagatggag | cgaagcagcc | 10080 |
| cacagtcgcc | atctggtggt | cacagcggt | gtccgcaggt | tccggctccg | ggcagccatg | 10140 |
| ctggaaggct | gggctggggc | tggtgttggg | ggacatctgc | ccggcatcat | tcactccctg | 10200 |
| cccacgtgtc | tgcgcctcac | ctcccagact | ccccggcccc | ccagcttggg | acccagcttg | 10260 |
| ggaccaggct | tctctgagtc | atggctgcgc | atagggctg | cttcataaat | gcttatgaat | 10320 |
| aaacctccct | tgggtgaaac | gaaggcg | cttcttgtt | tccagaggtt | tcccccctcc | 10380 |
| ccccccgtc | gcccaagaa | agaagactgg | gatcagagac | ctcagcttcc | atttccgcgt | 10440 |
| tgccacttct | ganccgtgta | ctttggcca | attctattta | ctgtttcgga | ncctacacgg | 10500 |
| ncctttcct | naaataggaa | caataaacca | ggggcacctt | tgacncactg | tgttagtancc | 10560 |
| aatttgcga | taantttttt | taaaagatta | aattaatcng | ataaaatt | | 10607 |

<210> 63
<211> 1176
<212> DNA
<213> Felis catus

| | | | | | | | |
|----------|------------|-------------|------------|------------|------------|------------|-----|
| <400> 63 | atgggacccc | gggcccaggga | agtctgctgc | ttcatcatcc | tgccgcggct | cctggctgag | 60 |
| | ccggctgaga | actcagactt | ctacttggct | ggggattact | tcctcggcgg | cctcttcacc | 120 |
| | ctccatgcca | acgtgaaggg | catcgtccac | ctcaacctcc | tgcaggtgcc | ccagtgc | 180 |
| | gagtatgaaa | taaagggtgtt | gggctacat | ctcatgcagg | ccatgtgtt | tgcaggggg | 240 |
| | gagatcaata | gccagagcag | cctgctgcct | ggcgtgctgc | tgggctacaa | aatgggtgat | 300 |
| | gtcagctaca | tctccaacaa | tgtccagccc | gtgctccact | tcccgcaaa | ggaggactgt | 360 |
| | tccttgc | tccaggagga | ctacagccac | tgtgtcccc | gtgtggtggc | tgtcattgg | 420 |
| | cctggcaact | ctgagtcac | tgtgactgt | gcccgc | tctctctt | cctc | 480 |
| | cagatcacct | acagcgccat | cagtgacgag | ctacggaca | agcagcgctt | cccgccctt | 540 |
| | ctgcccacag | cgccggcgc | cgatcaccag | atcgaggcca | tggtgcagct | gatgttgc | 600 |

MON-0301.ST25.txt

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|------|
| ttccgcggaa | actggatcat | cgcgctggtg | agcagcggcg | actgcggccg | cgacgacagc | 660 |
| cagctgctca | gcgatcgccc | ggccggcggc | gacacctgca | tcgccttccg | ggagacgctg | 720 |
| cccatgcccc | agccaaacca | ggcggtgacg | cagtgggagc | gccggcgct | gaaggccatc | 780 |
| gtggacgagc | agcagcggca | gagctctgcg | cgcgtcgtgg | tcctgctgtc | gccaaagctg | 840 |
| gtcctgcaca | acttcttccg | cgaggtgctc | cgcagaacc | tcacggcgt | cgtgcggatc | 900 |
| gcctccgagt | cctggccat | cgacccggtc | ctgcacgaca | ggcccacgcg | ctgcacagcc | 960 |
| tcctgggctg | caccagacc | agcagctccg | ggtcgcttat | ccctggcagg | tgaggccccca | 1020 |
| cccacggaga | gtcgccccca | cacacgcagg | cgccgccaca | gccctgagtg | gttgccatgg | 1080 |
| agaccactgc | cctgctctag | cgtccccctc | tctggccggg | tcctggcaa | actggcgaaa | 1140 |
| gaggccaggg | gacgtaccct | gtccccagac | acataa | | | 1176 |

<210> 64

<211> 391

<212> PRT

<213> Felis catus

<400> 64

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Pro | Arg | Ala | Arg | Glu | Val | Cys | Cys | Phe | Ile | Ile | Leu | Pro | Arg |
| 1 | | | | | | 5 | | | 10 | | | | 15 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Ala | Glu | Pro | Ala | Glu | Asn | Ser | Asp | Phe | Tyr | Leu | Ala | Gly | Asp |
| | | | 20 | | | | | 25 | | | | | 30 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Phe | Leu | Gly | Gly | Leu | Phe | Thr | Leu | His | Ala | Asn | Val | Lys | Gly | Ile |
| | | | 35 | | | | 40 | | | | | 45 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | His | Leu | Asn | Leu | Leu | Gln | Val | Pro | Gln | Cys | Lys | Glu | Tyr | Glu | Ile |
| | | | 50 | | | 55 | | | | 60 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Val | Leu | Gly | Tyr | Asp | Leu | Met | Gln | Ala | Met | Cys | Phe | Ala | Gly | Glu |
| 65 | | | | | 70 | | | 75 | | | | 80 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Ile | Asn | Ser | Gln | Ser | Ser | Leu | Leu | Pro | Gly | Val | Leu | Leu | Gly | Tyr |
| | | | 85 | | | | 90 | | | | | 95 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Met | Val | Asp | Val | Ser | Tyr | Ile | Ser | Asn | Asn | Val | Gln | Pro | Val | Leu |
| | | | 100 | | | | 105 | | | | | 110 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Phe | Pro | Ala | Lys | Glu | Asp | Cys | Ser | Leu | Pro | Ile | Gln | Glu | Asp | Tyr |
| | | | 115 | | | | 120 | | | | 125 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | His | Cys | Val | Pro | Arg | Val | Val | Ala | Val | Ile | Gly | Pro | Gly | Asn | Ser |
| | | | 130 | | | 135 | | | | 140 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Ser | Thr | Val | Thr | Val | Ala | Arg | Phe | Leu | Ser | Leu | Phe | Leu | Leu | Pro |
| 145 | | | | | 150 | | | | 155 | | | | 160 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Ile | Thr | Tyr | Ser | Ala | Ile | Ser | Asp | Glu | Leu | Arg | Asp | Lys | Gln | Arg |
| | | | | | 165 | | | 170 | | | | 175 | | | |

Phe Pro Ala Leu Leu Pro Thr Ala Pro Gly Ala Asp His Gln Ile Glu
180 185 190

Ala Met Val Gln Leu Met Leu Tyr Phe Arg Arg Asn Trp Ile Ile Ala
195 200 205

Leu Val Ser Ser Gly Asp Cys Gly Arg Asp Asp Ser Gln Leu Leu Ser
210 215 220

Asp Arg Pro Ala Gly Gly Asp Thr Cys Ile Ala Phe Arg Glu Thr Leu
225 230 235 240

Pro Met Pro Gln Pro Asn Gln Ala Val Thr Gln Trp Glu Arg Arg Arg
245 250 255

Leu Lys Ala Ile Val Asp Glu Gln Gln Arg Gln Ser Ser Ala Arg Val
260 265 270

Val Val Leu Leu Ser Pro Lys Leu Val Ile His Asn Phe Phe Arg Glu
275 280 285

Val Leu Arg Gln Asn Leu Thr Gly Val Val Arg Ile Ala Ser Glu Ser
290 295 300

Trp Ala Ile Asp Pro Val Leu His Asp Arg Pro Thr Arg Cys Thr Ala
305 310 315 320

Ser Trp Ala Ala Pro Arg Pro Ala Ala Pro Gly Arg Leu Ser Leu Ala
325 330 335

Gly Glu Ala Pro Pro Thr Glu Ser Arg Gly His Thr Arg Arg Arg
340 345 350

His Ser Pro Glu Trp Leu Pro Trp Arg Pro Leu Pro Cys Ser Ser Val
355 360 365

Pro Leu Ser Gly Arg Val Leu Gly Lys Leu Ala Gly Glu Ala Arg Gly
370 375 380

Arg Thr Leu Ser Pro Asp Thr
385 390

<210> 65
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 65
taaacaactc cacggccctg ctgc

MON-0301.ST25.txt

<210> 66
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 66
cccagggtga tggggcag cagg

24

<210> 67
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 67
gctgttatg cggtggccca tggc

24

<210> 68
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 68
ccaggagctg gtggaggcca tggg

24

<210> 69
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 69
tgctgaccaa cctgactggc aagg

24

<210> 70
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 70
tctgaggcga cccacacattt gccaa

24

<210> 71
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 71
ccagttcagc taaaacataaa tgtag

24

<210> 72
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 72
gccactggat ttgggtctca ttta

24

<210> 73
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 73
agctaacacg ctgctgctgc tgct

24

<210> 74
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 74
agcagtcccc agcagcagca gcag

24

<210> 75
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 75
tgtgtcacct tcagcctgct cttc

24

<210> 76
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 76
tccaggacac gaagttgaag agca

24

<210> 77
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 77
tacttcggcc ccaagtgcta catg

24

<210> 78
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 78
ccgggttagaa gaggatcatg tagc

24

<210> 79
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 79
tggtcaccat cgtggacctc ttgg

24

<210> 80
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 80
aggttgagca cagtgaccaa gagg

24

<210> 81
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 81
accaactaca acgaggccaa gttc

24

<210> 82
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 82
tcatgctgag ggtgatgaac ttgg

24

<210> 83
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 83

tccgagtcct gggccatcga cccg

24

<210> 84

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 84

tgagggttgtg caggaccggg tcga

24

<210> 85

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 85

tacaacctca tgcaggccat gcgc

24

<210> 86

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 86

tctcctccac cgcgaaagcgc atgg

24

<210> 87

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 87

atcaccatcc agagcgtgcc catc

24

<210> 88

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 88

actcactgaa gcccgaggatg ggca

24

<210> 89

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 89
accaccacgt cgaggccatg gtgc 24

<210> 90
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 90
aagtgcagca tcagctgcac catg 24

<210> 91
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 91
tcrgacttct acctgcctgg rga 23

<210> 92
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 92
cttcacgttg gcatggaggg 20

<210> 93
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 93
tacctcctgg gtggccttt c 21

<210> 94
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 94
tcttgcacwk gggcacctgc 20

<210> 95
<211> 22

MON-0301.ST25.txt

```

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 95
aggtgttggg ctacaacctt at 22

<210> 96
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 96
gggcakgttag tggctgtagt c 21

<210> 97
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 97
ggctacaacc tsatgcaggc ca 22

<210> 98
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 98
gagttgtcag ggccaaatgac cg 22

<210> 99
<211> 2598
<212> DNA
<213> Felis catus

<400> 99
atgccccggcc tcgctctcct gggcctcacg gctctcctgg gcctcacggc tctcttggac 60
cacggggagg ggcacacgtc ctgcttgta cagcagacta ggatgcaggg ggactatgtg 120
ctgggtgggc tcttccctct gggctctgcc gagggatcag gtcttggcg cgggctgcag 180
cccaatgcca ccgtgtgcac caggttctcg tctctggcc tgctctggc gctggccgtg 240
aagatggcgg tggaggagat caacaacggg tcggccctgc tgcccggct gcacctggc 300
tatgacactt ttgacacgtt ttcagagccc atggtgccca tgaagccca cctcggttc 360
atggccaaag caggcagctg cagcattgcc gcctactgca attacacaca gtaccagccc 420
cgcggtgtgg ccgtcatcg gccccactcg tctgagctcg ccctcggtcac cggcaagttc 480
ttcagcttct tccttggcc tcaggtcaac tacggcgcca gcaccgaccg gctgagcaac 540

```

MON-0301.ST25.txt

| | |
|---|------|
| cgggagatct tcccgtcctt cttccgcacg gtgcccagcg accaggtca ggtggcggcc | 600 |
| atggtgaggc tgctggagga gctcggtgg aactgggtgg cggcggtggg tagtgacgac | 660 |
| gagtatggcc ggcaggccc ggccttc tccggctgg ccagcgcag gggcatctgc | 720 |
| atcgccatg agggcctggt gccactgccg ccagggcagcc tgcggctggg cgccctacag | 780 |
| ggcctgctgc gccagggtgaa ccagagcagc gtgcagggtgg tggtgctgtt ctccctccgc | 840 |
| cacgcggccc gcaccctt cagctacagc atccgctgca agctctcacc caaggtgtgg | 900 |
| gtggccagcg aggccctggct gacctcagac ctggcatgca cgctgcccgg catgcctggg | 960 |
| gtggccaccc gcttggccct ggccgctgac cctgccttgc gcgcctcgct ggacgctgaa | 1020 |
| cagccaggcc tggaggagca cgtgggtggg ccacgctgcc cccaatgtga ccacgtcacg | 1080 |
| ctagagaacc tatctgcggg gctgctgcac caccagacct tcgctgccta cgccgctgtg | 1140 |
| tatggcgtgg cccaagccct tcacaacaca ctgcgctgca atgcctcggg ctgccccagg | 1200 |
| cgggagcctg tgccggccctg gcagctccta gagaacatgt acaacgttag cttccgtgt | 1260 |
| cgcggcctgg cactgcagtt cgacgcagc gggAACGTGA acgtggatta cgacactgaaa | 1320 |
| ctgtgggtgt ggcaggaccc gacgcccgg ctgcgcaccc taggcaccc ttcaaggccgc | 1380 |
| ctggagctct ggcgctctca gatgtgtgg cacacgcggg ggaaggcagca gcccgtgtcc | 1440 |
| cagtgtccc ggcagtgc aaaggccag gtgcgcccgc tgaagggttt ccactttgc | 1500 |
| tgttacaact gcgtggactg caaggcgggc agttatcagc gcaacccaga tgacctctc | 1560 |
| tgcacccagt gtgaccagga ccagtggtcc ccagacccggc gcacacgctg cttcccccgc | 1620 |
| aagccatgt tcctggcatg gggggagcca gctgtgtgc tactgctgc gctgtggct | 1680 |
| ctggcgctgg gcctggcgct ggcagccctg gggctttcc tctggcactc ggacagcccg | 1740 |
| ctggttcagg cctcagggtgg gccacggggc tgctttggcc tggcttgcc tggctggc | 1800 |
| tgcctcagtg tcctctgtt ccctggccag ccaggccctg ccagctgcct ggcccgacag | 1860 |
| ccactgttcc acctcccact cactggctgc ctgagcacgt ttttcctgca agcggccggag | 1920 |
| atatttgtgg ggtcgagct gccaccaagc tgggctgaga agatgcgtgg ccgcctgcgg | 1980 |
| gggccttggg cctggctgg ggtgtgtt gctatgtgg cagaagccgc atttgtgtcc | 2040 |
| tggtaacctgg tagccttccc gccagaggtg gtgacggact ggcgggtact gcccacagag | 2100 |
| gcgcgttgtgc actgccacgt gcactcctgg atcagttcg gcctggtgca tgccactaac | 2160 |
| gccatgtgg ccttcctctg cttcctggc actttctgg tgcaagccgc gccaggccgc | 2220 |
| tacaatggtg cccgcggcc caccttgcc atgctggcct acttcatacac ctggatctcc | 2280 |
| tttgtgcccc tctttgccaa tgtgcacgtg gcctaccaggc ctgcgtgca gatgggcacc | 2340 |
| atccttcctct gtgccttggg tattcttagcc accttccacc tgcccaagtg ctacctgtgt | 2400 |
| ctgcagcggc cggagctcaa cacccctgag ttcttcctgg aagacaatgc cagacacag | 2460 |
| ggcagcagtt gggggcaggg gaggggagaa tcggggcaaa aacaagtgac acccgatcca | 2520 |
| gtgacactcac cgcaagtga | 2580 |
| | 2598 |

